



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Suzuki, Shintaro

(ii) TITLE OF INVENTION: Protocadherin Materials and Methods

(iii) NUMBER OF SEQUENCES: 115

(iv) CORRESPONDENCE ADDRESS:

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(C) CITY: Chicago

(D) STATE: Illinois

(E) COUNTRY: USA

(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: Patent In Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: 18 JUN 1998

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/263,161

(B) FILING DATE: 27 JUN 1994

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: 27866/34703

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AARSSNNNTNG ATRYGA

17

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTRCTRTTTRC GNNGNNN

17

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

AAGGGAGTGG ACTTGAGGA GCAGCCTGAG CTTAGTCTCA TCCTCACGGC TTTGGATGGA

60

GGGACTCCAT CCAGGTCTGG GACTGCATTG GTTCAAGTGG AAGTCATAGA TGCCAATGAC

120

AACGCACCGT A

131

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys Gly Val Asp Phe Glu Glu Gln Pro Glu Leu Ser Leu Ile Leu Thr
1 5 10 15

Ala Leu Asp Gly Gly Thr Pro Ser Arg Ser Gly Thr Ala Leu Val Gln
20 25 30

Val Glu Val Ile Asp Ala Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AAACGCATGG ATTCGAGGA GTCTTCCTCC TACCAAGATCT ATGTGCAAGC TACTGACCGG	60
GGACCAGTAC CCATGGCGGG TCATTGCAAG GTGTTGGTGG ACATTATAGA TGTGAACGAC	120
AACGCACCTA A	131

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Ala Met Asp Phe Glu Glu Ser Ser Ser Tyr Gln Ile Tyr Val Gln	15
1 5 10 15	
Ala Thr Asp Arg Gly Pro Val Pro Met Ala Gly His Cys Lys Val Leu	30
20 25 30	
Val Asp Ile Ile Asp Val Asn Asp Asn Ala Pro	40
35 40	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGCGACTGG ACTTTGAGAC CCTGCAGACC TTCAAGTTCA GCGTGGGTGC CACAGACCAT	60
GGCTCCCCCT CGCTCCGCAG TCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CCACAATGAC	120
AATGCCCA A	131

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys	Arg	Leu	Asp	Phe	Glu	Thr	Leu	Gln	Thr	Phe	Glu	Phe	Ser	Val	Gly
1					5					10				15	

Ala	Thr	Asp	His	Gly	Ser	Pro	Ser	Leu	Arg	Ser	Gln	Ala	Leu	Val	Arg
									20			25		30	

Val	Val	Val	Leu	Asp	His	Asn	Asp	Asn	Ala	Pro					
								35		40					

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGGGCCTGG ATTACGAGGC ACTGCAGTCC TTTCGAGTTCT ACGTGGCGC TACAGATGGA	60
GGCTCACCCG CGCTCAGCAG CCAGACTCTG GTGCGGATGG TGGTGCTGGA TGACAAACGAC	120
AACGCCCTA A	131

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Lys	Gly	Leu	Asp	Tyr	Glu	Ala	Leu	Gln	Ser	Phe	Glu	Phe	Tyr	Val	Gly
1					5					10				15	

Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr Leu Val Arg
 20 25 30

Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAGGCCTTG ATTTGAGGA TCAGAGAGAG TTCCAGCTAA CCGCTCATAT AAACGACGGA 60
 GGTACCCCGG TTTTGGCCAC CAACATCAGC GTGAACATAT TTGTTACTGA CCGCAATGAC 120
 AACGCCCGC A 131

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Ala Phe Asp Phe Glu Asp Gln Arg Glu Phe Gln Leu Thr Ala His
 1 5 10 15

Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn
 20 25 30

Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAGGCGGTGG ATTACGAAAT CACCAAGTCC TATGAGATAG ATGTTCAAGC CCAAGATCTG	60
GGTCCAATT CTATTCCCTGC TCATTGCAAA ATTATAATTA AGGTCGTGGA TGTCAACGAC	120
AACGCTCCCA A	131

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Ala Val Asp Tyr Glu Ile Thr Lys Ser Tyr Glu Ile Asp Val Gln			
1	5	10	15
Ala Gln Asp Leu Gly Pro Asn Ser Ile Pro Ala His Cys Lys Ile Ile			
20	25	30	
Ile Lys Val Val Asp Val Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TATGACCATG ATTACGAGAC AACCAAAGAA TATACACTGC GGATCCGGGC CCAGGATGGT	60
GGCCGGACTC CACTTCCAA CGTCTCCGGT CTAGTAACCG TGCAGGTCT AGACATCAAC	120
GACAATGCCA CCCCCA	135

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

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Tyr Asp His Asp Tyr Glu Thr Thr Lys Glu Tyr Thr Leu Arg Ile Arg
1           5           10           15

Ala Gln Asp Gly Gly Arg Thr Pro Leu Ser Asn Val Ser Gly Leu Val
20          25          30

Thr Val Gln Val Leu Asp Ile Asn Asp Asn Ala Pro
35          40

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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GGGGGGTCGA TTACGAGGAG AACGGCATGT TAGAGATCGA CGTGCAGGCC AGAGACCTAG 60
GACCTAACCC AATTCCAGCC CATTGCAAGG TCACAGTCAA GCTCATCGAC CGCAATGATA 120
ACGCCCCCA 129

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AAGGGGTTGG ACTACGAAGA CACCAAACTC CATGAGATTT ACATCCAGGC CAAAGACAAA	60
GGTGCCAATC CGGAAGGAGC GCATTGCAAA GTACTGGTAG AGGTTGTGGA CGTTAACGAC	120
AATGCCCTC A	131

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Lys Gly Leu Asp Tyr Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln			
1	5	10	15
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu			
20	25	30	
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGGGTTTGG ACTTGAGCA AGTAGATGTC TACAAATCC GCGTTGACGC GACGGACAAA	60
GGACACCCCTC CGATGGCAGG CCATTGCACT GTTTAGTGA GGGTATTGGA TGAAAACGAC	120
AATGCGCCTC T	131

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Lys Gly Leu Asp Phe Glu Gln Val Asp Val Tyr Lys Ile Arg Val Asp
1 5 10 15

Ala Thr Asp Lys Gly His Pro Pro Met Ala Gly His Cys Thr Val Leu
20 25 30

Val Arg Val Leu Asp Glu Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAGGGTATAG ACTTCGAGCA GATCAAGGAC TTCAGCTTTC AAGTGGAAGC CCGGGACGCC 60

GGCAGTCCCC AGGCGCTGTC CGGCAACTGC ACTGTCAACA TCTTGATAGT GGATCAGAAC 120

GACAACGCCCTAA 134

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Lys Gly Ile Asp Phe Glu Gln Ile Lys Asp Phe Ser Phe Gln Val Glu
1 5 10 15

Ala Arg Asp Ala Gly Ser Pro Gln Ala Leu Ala Gly Asn Thr Thr Val			
20	25	30	
Asn Ile Leu Ile Val Asp Gln Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCCGTTCG ACTATGAGCA AACCGCCAAAC ACGCTGGCAC AGATTGACGC CGTGCTGGAA	60
AAACAGGGCA GCAATAAATC GAGCATTCTG GATGCCACCA TTTTCCTGGC CGATAAAAAC	120
GACAATGCGC CAGA	134

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Lys Pro Phe Asp Tyr Glu Gln Thr Ala Asn Thr Leu Ala Gln Ile Asp			
1	5	10	15
Ala Val Leu Glu Lys Gln Gly Ser Asn Lys Ser Ser Ile Leu Asp Ala			
20	25	30	
Thr Ile Phe Leu Ala Asp Lys Asn Asp Asn Ala Pro			
35	40		

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGCGGCTGG ATTCGAACA GTTCCAGCAG CACAAGCTGC TCGTAAGGGC TGTTGATGGA	60
GGAATGCCGC CACTGAGCAG CGATGTGGTC GTCACTGTGG ATGTCACCGA CCTCAACGAT	120
AACGCGCCCT A	131

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Lys Arg Leu Asp Phe Glu Gln Phe Gln Gln His Lys Leu Leu Val Arg	
1 5 10 15	
Ala Val Asp Gly Gly Met Pro Pro Leu Ser Ser Asp Val Val Val Thr	
20 25 30	
Val Asp Val Thr Asp Leu Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAGGGGATAG ACTTGAGAG TGAGAATTAC TATGAATTG ATGTGCGGGC TCGCGATGGG	60
GGTTCTCCAG CCATGGAGCA ACATTGCAGC CTTCGAGTGG ATCTGCTGGA CGTAAATGAC	120
AACGCCCCAC T	131

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys	Gly	Ile	Asp	Phe	Glu	Ser	Glu	Asn	Tyr	Tyr	Glu	Phe	Asp	Val	Arg
1				5					10					15	
Ala	Arg	Asp	Gly	Gly	Ser	Pro	Ala	Met	Glu	Gln	His	Cys	Ser	Leu	Arg
								20				25		30	
Val	Asp	Leu	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro					
								35				40			

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAGGCATTGG ACTTTGAGGC CCGGCGACTG TATTCGCTGA CAGTCAGGC CACGGACCGA 60
 GGC GTGCCCT CGCTCACCGG GCGTGCCGAA GCGCTTATCC AGCTGCTAGA TGTCAACGAC 120
 AACGCACCCCA T 131

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AAGCCAATTG ATTACGAGGC AACTCCATAC TATAACATGG AAATTGTAGC CACAGACAGC	60
GGAGGTCTTT CGGGAAAATG CACTGTGTCT ATACAGGTGG TGGATGTGAA CGACAACGCC	120
CCCAA	125

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Lys Pro Ile Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Met Glu Ile Val	15
1 5 10	15
Ala Thr Asp Ser Gly Gly Leu Ser Gly Lys Cys Thr Val Ser Ile Gln	30
20 25	30
Val Val Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AAGCGGGTAG ACTTCGAAAT GTGCAAAGA TTTTACCTTG TGGTGGAAAGC TAAAGACGGA	60
GGCACCCAG CCCTCAGCAC GGCAGCCACT GTCAGCATCG ACCTCACAGA TGTGAATGAT	120

AACCCTCCTC GGTCAGCCA AGATGTCTAC AGTGCTGTCA TCAGTGAGGA TGCCTTAGAG	180
GGGGACTCTG TCATTCTGCT GATAGCAGAA GATGTGGATA GCAAGCCTAA TGGACAGATT	240
CGGTTTCCA TCGTGGGTGG AGATAGGGAC AATGAATTG CTGTCGATCC AATCTTGGGA	300
CTTGTGAAAG TTAAGAAGAA ACTGGACCGG GAGCGGGTGT CAGGATACTC CCTGCTCATC	360
CAGGCAGTAG ATAGTGGCAT TCCTGCAATG TCCTCAACGA CAACTGTCAA CATTGATATT	420
TCTGATGTGA ACGACAACGC CCCCC	446

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Lys Arg Val Asp Phe Glu Met Cys Lys Arg Phe Tyr Ileu Val Val Glu			
1	5	10	15
10	15		

Ala Lys Asp Gly Gly Thr Pro Ala Leu Ser Thr Ala Ala Thr Val Ser			
20	25	30	
30			

Ile Asp Leu Thr Asp Val Asn Asp Asn Pro Pro Arg Phe Ser Gln Asp			
35	40	45	
45			

Val Tyr Asp Ala Val Ile Ser Glu Asp Ala Leu Glu Gly Asp Ser Val			
50	55	60	
60			

Ile Leu Leu Ile Ala Glu Asp Val Asp Ser Lys Pro Asn Gly Gln Ile			
65	70	75	80
75	80		

Arg Phe Ser Ile Val Gly Gly Asp Arg Asp Asn Glu Phe Ala Val Asp			
85	90	95	
95			

Pro Ile Leu Gly Leu Val Lys Val Lys Lys Lys Leu Asp Arg Glu Arg			
100	105	110	
110			

Val Ser Gly Tyr Ser Leu Leu Ile Gln Ala Val Asp Ser Gly Ile Pro			
115	120	125	
125			

Ala Met Ser Ser Thr Thr Val Asn Ile Asp Ile Ser Asp Val Asn			
130	135	140	
140			

Asp Asn Ala Pro
145

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AAGGGGGTTG ATTATGAGAC AAACCCACGG CTACGACTGG TGCTACAGGC AGAGAGTGG 60
GGAGCCTTG CTTTCTCGGT GCTGACCCTG ACCCTTCAAG ATGCCAATGA CAATGCTCCC 120
CGTTTCCTGC AGCCTCACTA CGTGGCTTTC CTGCCAGAGT CCCGACCCCTT GGAAGGGCCC 180
CTGCTGCAGG TGGAAGCAGA CGACCTGGAT CAAGGCTCTG GAGGACAGAT CTCCTACAGT 240
CTGGCTGCAT CCCAGCCAGC ACGGGGCTTG TTCCATGTAG ACCCAGCCAC AGGCACTATC 300
ACTACCACAG CCATCCTGGA CCGGGAAATC TGGGCTGAAA CACGGCTGGT ACTGATGGCC 360
ACAGACAGAG GAAGCCCAGC ATTGGTGGGC TCAGCTACCC TGACAGTGAT GGTCACTCGAT 420
ACCAACGACA ATGCTCCCCCT 440

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys	Gly	Val	Asp	Tyr	Glu	Thr	Asn	Pro	Arg	Leu	Arg	Leu	Val	Leu	Gln
1				5					10					15	
Ala	Glu	Ser	Gly	Gly	Ala	Phe	Ala	Phe	Ser	Val	Leu	Thr	Leu	Thr	Leu
									25					30	
Gln	Asp	Ala	Asn	Asp	Asn	Ala	Pro	Arg	Phe	Leu	Gln	Pro	His	Tyr	Val
								35				40		45	
Ala	Phe	Leu	Pro	Glu	Ser	Arg	Pro	Leu	Glu	Gly	Pro	Leu	Leu	Gln	Val
								50				55		60	
Glu	Ala	Asn	Asp	Leu	Asp	Gln	Gly	Ser	Gly	Gly	Gln	Ile	Ser	Tyr	Ser
								65				70		75	
Leu	Ala	Ala	Ser	Gln	Pro	Ala	Arg	Gly	Leu	Phe	His	Val	Asp	Pro	Ala
									85			90			95

Thr Gly Thr Ile Thr Thr Ala Ile Leu Asp Arg Glu Ile Trp Ala
 100 105 110
 Glu Thr Arg Leu Val Leu Met Ala Thr Asp Arg Gly Ser Pro Ala Leu
 115 120 125
 Val Gly Ser Ala Thr Leu Thr Val Met Val Ile Asp Thr Asn Asp Asn
 130 135 140
 Ala Pro
 145

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

AAGGTCTCGA TTATGAGGCA ACTCCATATT ATAACGTGGA AATTGTAGCC ACAGATGGTG	60
GGGGCCTTTC AGGAAAATGC ACTGTGGCTA TAGAAGTGGT GGATGTGAAC GACGGCGCTC	120
CAAT	124

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Gly Leu Asp Tyr Glu Ala Thr Pro Tyr Tyr Asn Val Glu Ile Val	15
1 5 10	
Ala Thr Asp Gly Gly Ala Phe Asp Glu Asn Cys Thr Val Ala Ile Glu	30
20 25	
Val Val Asp Val Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Asp Xaa Asn Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Xaa Asp Glu Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Xaa Asn Asp Asn Xaa Pro Xaa Phe
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AAGCGGATGG ATTTGAAGA CACCAAAC	TC CATGAGATT	ACATCCAGGC CAAAGACAAA	60
GGTGCCAATC CCGAAGGAGC GCATTGCAA	AA GTACTTGTAG	AGGTTGTAGA CGTAAACGAC	120
AACGCC	CC	CAG T	131

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Arg Met Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln							
1	5	10	15				
Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu							
20	25	30					
Val Glu Val Val Asp Val Asn Asp Asn Ala Pro							
35	40						

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

AAGGCTTGG ATTACGAGGA TCAGAGAGAG TTCCAACTAA CAGCTCATAT AAACGACGGA	60		
GGTACCCAG TCTTAGCCAC CAACATCAGC GTAACGTAT TTGTTACTGA CCGCAATGAT	120		
AACGCC	CC	CCT A	131

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys	Ala	Leu	Asp	Tyr	Glu	Asp	Gln	Arg	Glu	Phe	Gln	Leu	Thr	Ala	His
1				5				10					15		
Ile Asn Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn															
20 25 30															
Val Phe Val Thr Asp Arg Asn Asp Asn Ala Pro															
35 40															

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AAGCGCTTGG	ACTACGAGGA	GAGTAACAAT	TATGAAATT	ACGTGGATGC	TACAGATAAA	60
GGATACCCAC	CTATGGTTGC	TCACTGCACC	GTACTCGTGG	GAATCTTGG	TGAAAATGAC	120
AACGCACCCA T						131

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Lys	Arg	Leu	Asp	Tyr	Glu	Glu	Ser	Asn	Asn	Tyr	Glu	Ile	His	Val	Asp
1				5				10				15			
Ala Thr Asp Lys Gly Tyr Pro Pro Met Val Ala His Cys Thr Val Leu															
20 25 30															
Val Gly Ile Leu Asp Glu Asn Asp Asn Ala Pro															
35 40															

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

AAACCGGTGG ACTACGAGAA AGTCAAAGAC TATACCATCG AGATCGTGGC TGTGGATTCC 60
GGCAACCCCTC CACTCTCTAG CACCAAATCC CTCAAGGTGC AGGTGGTAGA CGTCAACGAT 120
AACGCCCTC T 131

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

AAGCCTTTG ATTCGAGGA CACCAAAC TC CATGAGATT ACATCCAGGC CAAAGACAAG 60
GGCGCCAATC CCGAAGGGAGC ACATTGCAAA GTGTTGGTGG AGGTTGTGGA TGTGAACGAC 120

AATGCCCTC A

131

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Pro Phe Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr Ile Gln
5 10 15

Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys Val Leu
20 25 30

Val Glu Val Val Asp Val Asn Asp Asn Ala Pro
35 40

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

AAAGGTGTCG ATTACGAGGT GAGTCCACGG CTGCGACTGG TGCTGCAGGC AGAGAGTCGA 60
GGAGCCCTTG CCTTCACTGT GCTGACCCCTG ACCCTGCAAG ATGCCAACGA CAACGCCCG 120
AG 122

AG

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys Gly Val Asp Tyr Glu Val Ser Pro Arg Leu Arg Leu Val Leu Gln
 1 5 10 15

Ala	Glu	Ser	Arg	Gly	Ala	Phe	Ala	Phe	Thr	Val	Leu	Thr	Leu
20						25						30	
Gln	Asp	Ala	Asn	Asp	Asn	Ala	Pro						
35						40							

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

AAAGGGATTG	ATTACGAGCA	GTTGAGAGAC	CTACAGCTGT	GGGTGACAGC	CAGCGACAGC	60
GGGGACCCGC	CTCTTAGCAG	CAACGTGTCA	CTGAGCCTGT	TTGTGCTGGA	CCAGAACGAC	120
AACGCC	CCCC	T				131

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Lys	Gly	Ile	Asp	Tyr	Glu	Gln	Leu	Arg	Asp	Leu	Gln	Leu	Trp	Val	Thr
1					5								10		15
Ala	Ser	Asp	Ser	Gly	Asp	Pro	Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser
													25	30	
Leu	Phe	Val	Leu	Asp	Gln	Asn	Asp	Asn	Ala	Pro					
35					40										

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AAGGCGGTG	ATTTGAGCG	CACATCCTCT	TATCAACTCA	TCATTCAGGC	CACCAATATG	60
GCAGGAATGG	CTTCCAATGC	TACAGTCAAT	ATTCAGATTG	TTGATGAAAA	CGACAAACGCC	120
CCCCA						125

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Lys	Ala	Val	Asp	Phe	Glu	Arg	Thr	Ser	Ser	Tyr	Gln	Leu	Ile	Ile	Gln
1				5	..				10					15	
Ala	Thr	Asn	Met	Ala	Gly	Met	Ala	Ser	Asn	Ala	Thr	Val	Asn	Ile	Gln
			20					25					30		
Ile	Val	Asp	Glu	Asn	Asp	Asn	Ala	Pro							
		35				40									

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAACGGCTAG	ACTTTGAAAA	GATACAAAAA	TATGTTGTAT	GGATAGAGGC	CAGAGATGGT	60
GGTTTCCCTC	CTTTCTCCTC	TTACGAGAAA	CTTGATATAA	CAGTATTAGA	TGTCAACGAT	120
AACGCGCCTA	A					131

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 43 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

AAGGGACTCG ACTACGAGGA TCGGCAGGAA TTTGAATTAA CAGCTCATAT CAGCGATGGG	60
GGCACCCCGG TCCTAGCCAC CAACATCAGC GTGAACATAT TTGTCACTGA TCGCAACGAT	120
AATGCCCGG T	131

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Lys Gly Leu Asp Tyr Glu Asp Arg Arg Glu Phe Glu Leu Thr Ala His	15
1 5 10	15
Ile Ser Asp Gly Gly Thr Pro Val Leu Ala Thr Asn Ile Ser Val Asn	30
20 25	30
Ile Phe Val Thr Asp Arg Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAGGGTTTGG ACTACGAGAC CACACAGGCC TACCAAGCTCA CGGTCAACGC CACAGATCAA	60
GACAACACCA GGCCTCTGTC CACCCTGGCC AACTTGGCCA TCATCATCAC AGATGTCCAG	120

GACATGGACC CCATCTTCAT CAACCTGCCT TACAGCACCA ACATCTACGA GCATTCTCCT 180
CCGGGCACGA CGGTGCGCAT CATCACCGCC ATAGACCAGG ATCAAGGACG TCCCCGGGGC 240
ATTGGCTACA CCATCGTTTC AGGGAATACC AACAGCATCT TTGCCCTGGA CTACATCAGC 300
GGAGTGCTGA CCTTGAATGG CCTGCTGGAC CGGGAGAACCC CCGTGTACAG CCATGGCTTC 360
ATCCTGACTG TGAAGGGCAC GGAGCTGAAC GATGACCGCA CCCCCATCTGA CGCTACAGTC 420
ACCACGACCT TCAATATCCT GGTTATTGAC ATCAACGACA ACGCCCCACT 470

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Lys Gly Leu Asp Tyr Glu Thr Thr Gln Ala Tyr Gln Leu Thr Val Asn
 1 5 10 15
 Ala Thr Asp Gln Asp Asn Thr Arg Pro Leu Ser Thr Leu Ala Asn Leu
 20 25 30
 Ala Ile Ile Ile Thr Asp Val Gln Asp Met Asp Pro Ile Phe Ile Asn
 35 40 45
 Leu Pro Tyr Ser Thr Asn Ile Tyr Glu His Ser Pro Pro Gly Thr Thr
 50 55 60
 Val Arg Ile Ile Thr Ala Ile Asp Gln Asp Gln Gly Arg Pro Arg Gly
 65 70 75 80
 Ile Gly Tyr Thr Ile Val Ser Gly Asn Thr Asn Ser Ile Phe Ala Leu
 85 90 95
 Asp Tyr Ile Ser Gly Val Leu Thr Leu Asn Gly Leu Leu Asp Arg Glu
 100 105 110
 Asn Pro Leu Tyr Ser Gly Gly Phe Ile Leu Thr Val Lys Gly Thr Glu
 115 120 125
 Leu Asn Asp Asp Arg Thr Pro Ser Asp Ala Thr Val Thr Thr Thr Phe
 130 135 140
 Asn Ile Leu Val Ile Asp Ile Asn Asp Asn Ala Pro
 145 150 155

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AAGGGGGTCT ATTACGAGGT ACTACAGGCC TTTGAGTTCC ACGTGAGCGC CACAGACCGA	60
GGCTCACCGG GGCTCAGCAG CCAGGCTCTG GTGCGCGTGG TGGTGCTGGA CGACAATGAC	120
AACGCTCCCG T	131

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Lys Gly Val Asp Tyr Glu Val Leu Gln Ala Phe Glu Phe His Val Ser	
1	5
	10
	15
Ala Thr Asp Arg Gly Ser Pro Gly Leu Ser Ser Gln Ala Leu Val Arg	
20	25
	30
Val Val Val Leu Asp Asp Asn Asp Asn Ala Pro	
35	40

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

AAGGGGCTGG ATTATGAGCA GTTCCAGACC CTACAACTGG GAGTGACCGC TAGTGACAGT	60
GGAAACCCAC CATTAAGAAG CAATATTCA CTGACCCTTT TCGTGCTGGA CCAGAATGAT	120

AACGCCCAA A

131

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Lys	Gly	Leu	Asp	Tyr	Glu	Gln	Phe	Gln	Thr	Leu	Gln	Leu	Gly	Val	Thr
1					5				10					15	

Ala	Ser	Asp	Ser	Gly	Asn	Pro	Pro	Leu	Arg	Ser	Asn	Ile	Ser	Leu	Thr
20							25						30		

Leu	Phe	Val	Leu	Asp	Gln	Asn	Asp	Asn	Ala	Pro					
35						40									

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

AAGCGGGTTG	ATTACGAGGA	TGTCCAGAAA	TACTCGCTGA	GCATTAAGGC	CCAGGATGGG		60
CGGCCCGCGC	TCATCAATTG	TTCAGGGGTG	GTGTCTGTGC	AGGTGCTGGG	TGTCAACGAC		120
AATGCCCGG	A						131

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Lys	Arg	Val	Asp	Tyr	Glu	Asp	Val	Gln	Lys	Tyr	Ser	Leu	Ser	Ile	Lys
1					5				10					15	

Ala Gln Asp Gly Arg Pro Pro Leu Ile Asn Ser Ser Gly Val Val Ser
 20 25 30
 Val Gln Val Leu Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

AAACCGGTAG ACTTGAGCT ACAGCAGTTC TATGAAGTAG CTGTGGTGGC TTGGAACCTCT 60
 GAGGGATTTC ATGTCAAAAG GGTCATTAAA GTGCAACTTT TAGATGACAA CGACAATGCC 120
 CCGAT 125

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Pro Val Asp Phe Glu Leu Gln Gln Phe Tyr Glu Val Ala Val Val
 1 5 10 15
 Ala Trp Asn Ser Glu Gly Phe His Val Lys Arg Val Ile Lys Val Gln
 20 25 30
 Leu Leu Asp Asp Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGGGATTAG ATTTGAAAC TTTGCCATT TACACATTGA TAATACAAGG AACTAACATG	60
GCTGGTTTGT CCACTAATAC AACGGTTCTA GTTCACTTGC AGGATGAGAA TGATAACGCC	120
	125
CCAAA	

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 41 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Lys Gly Leu Asp Phe Glu Thr Leu Pro Ile Tyr Thr Leu Ile Ile Gln	
1	5
	10
	15
Gly Thr Asn Met Ala Gly Leu Ser Thr Asn Thr Thr Val Leu Val His	
20	25
	30
Leu Gln Asp Glu Asn Asp Asn Ala Pro	
35	40

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 134 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

AAGCGGGCGG ATTCGAGGC GATCCGGAG TACAGTCTGA GGATCAAAGC GCAGGACGGG	60
GGCGGCCCTC CCCTCAGCAA CACCACGGGC ATGGTCACAG TGCAGGTCGT GGACGTCAAT	120
	134
GACAACGCAC CCCT	

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 44 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AAGGGGATCG ATTATGAGGA TCAGGTCTCT TACACATTAG CAGTAACAGC ACATGACTAT	60
GGCATCCCTC AAAATCAGA CACTACCTAT TTGGAAATCT TAGTAATTGA TGTAAACGAC	120
AACGCGCCCC A	131

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Lys Gly Ile Asp Tyr Glu Asp Gln Val Ser Tyr Thr Leu Ala Val Thr	15
1	5
Ala His Asp Tyr Gly Ile Pro Gln Lys Ser Asp Thr Thr Tyr Leu Glu	30
20	25
Ile Leu Val Ile Asp Val Asn Asp Asn Ala Pro	
35	40

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

AAAGGGTTAG ATTCGAGGG CACTAAAGAT TCAGCGTTA AAATAGTGGC AGCTGACACA	60
GGGAAGCCCA GCCTCAACCA GACAGCCCTG GTGAGAGTAG AGCTGGAGGA TGAGAACGAC	120

AACGCCCAA T

131

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Lys	Gly	Leu	Asp	Phe	Glu	Gly	Thr	Lys	Asp	Ser	Ala	Phe	Lys	Ile	Val
1				5				10					15		

Ala	Ala	Asp	Thr	Gly	Lys	Pro	Ser	Leu	Asn	Gln	Thr	Ala	Leu	Val	Arg
			20					25				30			

Val	Glu	Leu	Glu	Asp	Glu	Asn	Asp	Asn	Ala	Pro					
			35			40									

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AAGGGTGTGG	ATTTTGAAAG	TGTGCGTAGC	TACAGGCTGG	TTATTCGTGC	TCAAGATGGA	60
GGCAGCCCCCT	CCAGAAGTAA	CACCACCCAG	CTCTGGTCA	ACGTCATCGA	TCGAATGACA	120
ATGCGCCGCT						130

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Lys	Gly	Val	Asp	Phe	Glu	Ser	Val	Arg	Ser	Tyr	Arg	Leu	Val	Ile	Arg
1				5				10				15			

Ala Gln Asp Gly Gly Ser Pro Ser Arg Ser Asn Thr Thr Gln Leu Leu
 20 25 30

Val Asn Val Ile Asp Val Asn Asp Asn Ala Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

AAGGGTGTGG ACTTCGAGCT GACACATCTG TATGAGATTT GGATTGAGGC TGCCGATGGA	60
GACACGCCAA GTCTGCGTAG TGTAACTCTT ATAACGCTCA ACGTAACGGA TGCCAATGAC	120
AATGCTCCCA A	131

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Gly Val Asp Phe Glu Leu Thr His Leu Tyr Glu Ile Trp Ile Glu	
1 5 10 15	
Ala Ala Asp Gly Asp Thr Pro Ser Leu Arg Ser Val Thr Leu Ile Thr	
20 25 30	
Leu Asn Val Thr Asp Ala Asn Asp Asn Ala Pro	
35 40	

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CAAGCGTTT GATTTGAAG AGACAAGTAG ATATGTGTTG AGTGTGGAAG CTAAGGATGG 60
AGGAGTACAC ACAGCTCACT GTAATGTTCA AATAGAAATT GTTGACGAGA ATGACAATGC 120
CCCAGAGGTG ACATTCATGT CCTTCTCTAA CCAGATTCCA GAGGATTCAAC ACCTTGGAAC 180
TGTAATAGCC CTCATAAAAG TGCGAGACAA GGATTCTGGG CAAAATGGCA TGGTGACATG 240
CTATACTCAG GAAGAAGTTC CTTTCAAATT AGAATCCACC TCGAAGAATT ATTACAAGCT 300
GGTGATTGCT GGAGCCCTAA ACCGGGAGCA GACAGCAGAC TACAACGTCA CAATCATAGC 360
CACCGACAAG GGCACAAACAG CCCTTCCTC CAGGACAAGC ATCACCCCTGC ACATCTCCGA 420
CATCAACGTAAATGCCCG T 441

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

AAGCGAGTGG ATTACGAGGC CACTCGGAAT TATAAGCTGA GAGTTAAGGC TACTGATCTT GGGATTCCAC CGAGATCTTC TAACATGACA CTGTCATTC ATGTCCTTGA TGTTAACGAC AACGCTCCCT T	60 120 131
---	------------------

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Lys Arg Val Asp Tyr Glu Ala Thr Arg Asn Tyr Lys Leu Arg Val Lys 1 5 10 15 Ala Thr Asp Leu Gly Ile Pro Pro Arg Ser Ser Asn Met Thr Leu Phe 20 25 30	15 30
---	----------

Ile His Val Leu Asp Val Asn Asp Asn Ala Pro 35 40	
--	--

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..3572

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCTCTATTCTG ACATTCTCTT TGGATTGTTT TGCTATAACT TGAAATTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTCTGCT AATCTCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCC ACTCTTTCA CCTGAAATTC CTTTCCTTGG	180
TTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAAACCA ATCTCACTGC CTCCTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCACT	360
CGTTTCGTA CCTCTTCATG GTGATGGGA GCCCTTGGA GGTGGTGACT GTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGCG TGGAGTGCCTT GGAGGCGGCC CTCCTGATTC	480
TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG	530
Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG	578
Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu	
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG	626
Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT	674
Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC	722
Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC	770
Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT	818
Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT	866
Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT	914
Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT	962
Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC	1010
Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	
160 165 170	

CGT GAT GCT GGT CCC AAC GGT GTG GCA TCC TAT GAG CTG CAG GTG GCA Arg Asp Ala Gly Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala 175 180 185	1058
GAG GAC CAG GAG GAG AAG CAA CCA CAG CTC ATT GTG ATG GGC AAC CTG Glu Asp Gln Glu Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu 190 195 200	1106
GAC CGT GAG CGC TGG GAC TCC TAT GAC CTC ACC ATC AAG GTG CAG GAT Asp Arg Glu Arg Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp 205 210 215 220	1154
GGC GGC AGC CCC CCA CGC GCC ACG AGT GCC CTG CTG CGT GTC ACC GTG Gly Gly Ser Pro Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val 225 230 235	1202
CTT GAC ACC AAT GAC AAC GCC CCC AAG TTT GAG CGG CCC TCC TAT GAG Leu Asp Thr Asn Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu 240 245 250	1250
GCC GAA CTA TCT GAG AAT AGC CCC ATA GGC CAC TCG GTC ATC CAG GTG Ala Glu Leu Ser Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val 255 260 265	1298
AAG GCC AAT GAC TCA GAC CAA GGT GCC AAT GCA GAA ATC GAA TAC ACA Lys Ala Asn Asp Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr 270 275 280	1346
TTC CAC CAG GCG CCC GAA GTT GTG AGG CGT CTT CTT CGA CTG GAC AGG Phe His Gln Ala Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg 285 290 295 300	1394
AAC ACT GGA CTT ATC ACT GTT CAG GGC CCG GTG GAC CGT GAG GAC CTA Asn Thr Gly Leu Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu 305 310 315	1442
AGC ACC CTG CGC TTC TCA GTG CTT GCT AAG GAC CGA GGC ACC AAC CCC Ser Thr Leu Arg Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro 320 325 330	1490
AAG AGT GCC CGT GCC CAG GTG GTT GTG ACC GTG AAG GAC ATG AAT GAC Lys Ser Ala Arg Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp 335 340 345	1538
AAT GCC CCC ACC ATT GAG ATC CGG GGC ATA GGG CTA GTG ACT CAT CAA Asn Ala Pro Thr Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln 350 355 360	1586
GAT GGG ATG GCT AAC ATC TCA GAG GAT GTG GCA GAG GAG ACA GCT GTG Asp Gly Met Ala Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val 365 370 375 380	1634
GCC CTG GTG CAG GTG TCT GAC CGA GAT GAG GGA GAG AAT GCA GCT GTC Ala Leu Val Gln Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val 385 390 395	1682
ACC TGT GTG GTG GCA GGT GAT GTG CCC TTC CAG CTG CGC CAG GCC AGT Thr Cys Val Val Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser 400 405 410	1730

GAG ACA GGC AGT GAC AGC AAG AAG AAG TAT TTC CTG CAG ACT ACC ACC Glu Thr Gly Ser Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr 415 420 425	1778
CCG CTA GAC TAC GAG AAG GTC AAA GAC TAC ACC ATT GAG ATT GTG GCT Pro Leu Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala 430 435 440	1826
GTG GAC TCT GGC AAC CCC CCA CTC TCC AGC ACT AAC TCC CTC AAG GTG Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val 445 450 455 460	1874
CAG GTG GTG GAC GTC AAT GAC AAC GCA CCT GTC TTC ACT CAG AGT GTC Gln Val Val Asp Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val 465 470 475	1922
ACT GAG GTC GCC TTC CCG GAA AAC AAC AAG CCT GGT GAA GTG ATT GCT Thr Glu Val Ala Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala 480 485 490	1970
GAG ATC ACT GCC AGT GAT GCT GAC TCT GGC TCT AAT GCT GAG CTG GTT Glu Ile Thr Ala Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val 495 500 505	2018
TAC TCT CTG GAG CCT GAG CCG GCT GCT AAG GGC CTC TTC ACC ATC TCA Tyr Ser Leu Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser 510 515 520	2066
CCC GAG ACT GGA GAG ATC CAG GTG AAG ACA TCT CTG GAT CGG GAA CAG Pro Glu Thr Gly Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln 525 530 535 540	2114
CGG GAG AGC TAT GAG TTG AAG GTG GTG GCA GCT GAC CGG GGC AGT CCT Arg Glu Ser Tyr Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro 545 550 555	2162
AGC CTC CAG GGC ACA GCC ACT GTC CTT GTC AAT GTG CTG GAC TGC AAT Ser Leu Gln Gly Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn 560 565 570	2210
GAC AAT GAC CCC AAA TTT ATG CTG AGT GGC TAC AAC TTC TCA GTG ATG Asp Asn Asp Pro Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met 575 580 585	2258
GAG AAC ATG CCA GCA CTG AGT CCA GTG GGC ATG GTG ACT GTC ATT GAT Glu Asn Met Pro Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp 590 595 600	2306
GGA GAC AAG GGG GAG AAT GCC CAG GTG CAG CTC TCA GTG GAG CAG GAC Gly Asp Lys Gly Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp 605 610 615 620	2354
AAC GGT GAC TTT GTT ATC CAG AAT GGC ACA GGC ACC ATC CTA TCC AGC Asn Gly Asp Phe Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser 625 630 635	2402
CTG AGC TTT GAT CGA GAG CAA CAA AGC ACC TAC ACC TTC CAG CTG AAG Leu Ser Phe Asp Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys 640 645 650	2450

GCA GTG GAT GGT GGC GTC CCA CCT CGC TCA GCT TAC GTT GGT GTC ACC Ala Val Asp Gly Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr 655	660	665	2498
ATC AAT GTG CTG GAC GAG AAT GAC AAC GCA CCC TAT ATC ACT GCC CCT Ile Asn Val Leu Asp Glu Asn Asn Ala Pro Tyr Ile Thr Ala Pro 670	675	680	2546
TCT AAC ACC TCT CAC AAG CTG CTG ACC CCC CAG ACA CGT CTT GGT GAG Ser Asn Thr Ser His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu 685	690	695	2594
ACG GTC AGC CAG GTG GCA GCC GAG GAC TTT GAC TCT GGT GTC AAT GCC Thr Val Ser Gln Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala 705	710	715	2642
GAG CTG ATC TAC AGC ATT GCA GGT GGC AAC CCT TAT GGA CTC TTC CAG Glu Leu Ile Tyr Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln 720	725	730	2690
ATT GGG TCA CAT TCA GGT GCC ATC ACC CTG GAG AAG GAG ATT GAG CGG Ile Gly Ser His Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg 735	740	745	2738
CGC CAC CAT GGG CTA CAC CGC CTG GTG AAG GTC AGT GAC CGC GGC Arg His His Gly Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly 750	755	760	2786
AAG CCC CCA CGC TAT GGC ACA GCC TTG GTC CAT CTT TAT GTC AAT GAG Lys Pro Pro Arg Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu 765	770	775	2834
ACT CTG GCC AAC CGC ACG CTG CTG GAG ACC CTC CTG GGC CAC AGC CTG Thr Leu Ala Asn Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu 785	790	795	2882
GAC ACG CCG CTG GAT ATT GAC ATT GCT GGG GAT CCA GAA TAT GAG CGC Asp Thr Pro Leu Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg 800	805	810	2930
TCC AAG CAG CGT GGC AAC ATT CTC TTT GGT GTG GTG GCT GGT GTG GTG Ser Lys Gln Arg Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val 815	820	825	2978
GCC GTG GCC TTG CTC ATC GCC CTG GCG GTT CTT GTG CGC TAC TGC AGA Ala Val Ala Leu Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg 830	835	840	3026
CAG CGG GAG GCC AAA AGT GGT TAC CAG GCT GGT AAG AAG GAG ACC AAG Gln Arg Glu Ala Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys 845	850	855	3074
GAC CTG TAT GCC CCC AAG CCC AGT GGC AAG GCC TCC AAG GGA AAC AAA Asp Leu Tyr Ala Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys 865	870	875	3122
AGC AAA GGC AAG AAG AGC AAG TCC CCA AAG CCC GTG AAG CCA GTG GAG Ser Lys Gly Lys Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu 880	885	890	3170

GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905	3218
AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920	3266
CCA CCA GGC AGC CCT GAC CTG GGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940	3314
CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955	3362
CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970	3410
GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985	3458
CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG GTA GGC CAG CCC TTT Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe 990 995 1000	3506
CAG CTC AGC ACA CCC CAG CCC CTA CCC CAC CCC TAC CAC GGA GCC ATC Gln Leu Ser Thr Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile 1005 1010 1015 1020	3554
TGG ACC GAG GTG TGG GAG TGATGGAGCA GGTTTACTGT GCCTGCCCGT Trp Thr Glu Val Trp Glu 1025	3602
GTTGGGGGCC AGCCTGAGCC AGCAGTGGGA GGTGGGGCCT TAGTGCCTCA CCGGGCACAC GGATTAGGCT GAGTGAAGAT TAAGGGAGGG TGTGCTCTGT GGTCTCCTCC CTGCCCTCTC CCCACCTGGGG AGAGACCTGT GATTTGCCAA GTCCCTGGAC CCTGGACCAG CTACTGGGCC TTATGGGTTG GGGGTGGTAG GCAGGTGAGC GTAAGTGGGG AGGGAAATGG GTAAGAAGTC TACTCCAAAC CTAGGTCTCT ATGTCAGACC AGACCTAGGT GCTTCTCTAG GAGGGAAACA GGGAGACCTG GGGCCTGTG GATAACTGAG TGGGGAGTCT GCCAGGGAG GGCACCTTCC CATTGTGCCT TCTGTGTGTA TTGTGCATTA ACCTCTTCCT CACCACTAGG CTTCTGGGGC TGGGTCCCAC ATGCCCTTGA CCCTGACAAT AAAGTTCTCT ATTTTTGGAA AAAAAAAA AAAAAAA AAAAAAAA AA	3662 3722 3782 3842 3902 3962 4022 4082 4104

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly Gln Arg Leu Leu
 1 5 10 15

Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Ala Pro Ser Pro
 20 25 30

Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu Glu Gln Pro Pro
 35 40 45

Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly Phe Pro Asp Val
 50 55 60

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
 65 70 75 80

Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
 85 90 95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
 100 105 110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
 115 120 125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
 130 135 140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
 145 150 155 160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
 165 170 175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
 180 185 190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
 195 200 205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
 210 215 220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
 225 230 235 240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
 245 250 255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
 260 265 270

Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
 275 280 285
 Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
 290 295 300
 Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
 305 310 315 320
 Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
 325 330 335
 Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
 340 345 350
 Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
 355 360 365
 Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
 370 375 380
 Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
 385 390 395 400
 Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
 405 410 415
 Asp Ser Lys Lys Tyr Phe Leu Gln Thr Thr Thr Pro Leu Asp Tyr
 420 425 430
 Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
 435 440 445
 Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
 450 455 460
 Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
 465 470 475 480
 Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
 485 490 495
 Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
 500 505 510
 Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
 515 520 525
 Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
 530 535 540
 Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
 545 550 555 560
 Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
 565 570 575
 Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
 580 585 590

Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
 595 600 605
 Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
 610 615 620
 Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
 625 630 635 640
 Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
 645 650 655
 Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
 660 665 670
 Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
 675 680 685
 His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
 690 695 700
 Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
 705 710 715 720
 Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
 725 730 735
 Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His His Gly
 740 745 750
 Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro Pro Arg
 755 760 765
 Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu Ala Asn
 770 775 780
 Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr Pro Leu
 785 790 795 800
 Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys Gln Arg
 805 810 815
 Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val Ala Leu
 820 825 830
 Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg Glu Ala
 835 840 845
 Lys Ser Gly Tyr Gln Ala Gly Lys Glu Thr Lys Asp Leu Tyr Ala
 850 855 860
 Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys Gly Lys
 865 870 875 880
 Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu Asp Glu
 885 890 895
 Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp Ala Pro
 900 905 910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
 915 920 925
 Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
 930 935 940
 Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
 945 950 955 960
 Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
 965 970 975
 Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
 980 985 990
 Pro Lys Tyr Pro Ser Lys Gln Val Gly Gln Pro Phe Gln Leu Ser Thr
 995 1000 1005
 Pro Gln Pro Leu Pro His Pro Tyr His Gly Ala Ile Trp Thr Glu Val
 1010 1015 1020
 Trp Glu
 1025

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4705 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 115..2827

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG	117
Met	
1	
GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
5 10 15	
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
20 25 30	
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
35 40 45	

GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg 50 55 60 65	309
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg 70 75 80	357
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu 85 90 95	405
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu 100 105 110	453
AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn 115 120 125	501
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser 130 135 140 145	549
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp 150 155 160	597
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn 165 170 175	645
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr 180 185 190	693
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser 195 200 205	741
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser 210 215 220 225	789
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala 230 235 240	837
CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys 245 250 255	885
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu 260 265 270	933
GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala 275 280 285	981

GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290 295 300 305	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310 315 320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325 330 335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340 345 350	1173
GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val 355 360 365	1221
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu 370 375 380 385	1269
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser 390 395 400	1317
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu 405 410 415	1365
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr 420 425 430	1413
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile 435 440 445	1461
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Tyr Asp Val Tyr Ile 450 455 460 465	1509
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp 470 475 480	1557
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu 485 490 495	1605
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg 500 505 510	1653
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg 515 520 525	1701

CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val 530 535 540 545	1749
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp 550 555 560 560	1797
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu 565 570 575 575	1845
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val 580 585 590 590	1893
GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595 600 605 605	1941
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610 615 620 625	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630 635 640 640	2037
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645 650 655 655	2085
ACT GCT ACC CTC ACT GTG TCA GTC ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660 665 670 670	2133
GCC GAG TTC CCC TCT GGC TCT GCC CCC CGG GAG CAG AAA AAA AAT CTC Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn Leu 675 680 685 685	2181
ACC TTT TAT CTA CTT CTT TCT CTA ATC CTG GTT TCT GTG GGC TTC GTG Thr Phe Tyr Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe Val 690 695 700 705	2229
GTC ACA GTG TTC GGA GTA ATC ATA TTC AAA GTT TAC AAG TGG AAG CAG Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys Gln 710 715 720 720	2277
TCT AGA GAC CTA TAC CGA GCC CCG GTG AGC TCA CTG TAC CGA ACA CCA Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr Pro 725 730 735 735	2325
GGG CCC TCC TTG CAC GCG GAC GCC GTG CGG GGA GGC CTG ATG TCG CCG Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser Pro 740 745 750 750	2373
CAC CTT TAC CAT CAG GTG TAT CTC ACC ACG GAC TCC CGC CGC AGC GAC His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser Asp 755 760 765 765	2421

CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln 770 775 780 785	2469
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly 790 795 800	2517
GCA GAG AGC GCC CCT CCC GGA CAG CAA GCC CCG CCC AAC ACG GAC TGG Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp Trp 805 810 815	2565
CGT TTC TCT CAG GCC CAG AGA CCC GGC ACC AGC GGC TCC CAA AAT GGC Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn Gly 820 825 830	2613
GAT GAC ACC GGC ACC TGG CCC AAC AAC CAG TTT GAC ACA GAG ATG CTG Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met Leu 835 840 845	2661
CAA GCC ATG ATC TTG GCG TCC GCC AGT GAA GCT GCT GAT GGG AGC TCC Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser Ser 850 855 860 865	2709
ACC CTG GGA GGG GGT GCC GGC ACC ATG GGA TTG AGC GCC CGC TAC GGA Thr Leu Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr Gly 870 875 880	2757
CCC CAG TTC ACC CTG CAG CAC GTG CCC GAC TAC CGC CAG AAT GTC TAC Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val Tyr 885 890 895	2805
ATC CCA GGC AGC AAT GCA CAC T GACCAACGCA GCTGGCAAGC GGATGGCAAG Ile Pro Gly Ser Asn Ala His 900	2857
GCCCCAGCAGG TGGCAATGGC AACAAAGAAGA AGTCGGCAAG AAGGAGAAGA AGTAACATGG	2917
AGGCCAGGCC AAGAGCCACA GGGCAGCCTC TCCCCGAACC AGCCCAGCTT CTCCCTTACCT	2977
GCACCCAGGC CTCAGAGTTT CAGGGCTAAC CCCCAGAATA CTGGTAGGGG CCAAGGCATC	3037
TCCCTTGAA ACAGAAACAA GTGCCATCAC ACCATCCCTT CCCCAGGTGT AATATCCAAA	3097
GCAGTTCCGC TGGGAACCCC ATCCAATCAG TGGCTGTACC CATTGGGTA GTGGGGTTCA	3157
TGTAGACACC AAGAACCAATT TGCCACACCC CGTTTAGTTA CAGCTGAACC CTCCATCTTC	3217
CAAATCAATC AGGCCATCC ATCCCATGCC TCCCTCCTCC CCACCCACT CCAACAGTTC	3277
CTCTTTCCCG AGTAAGGTGG TTGGGGTGT GAAGTACCAA GTAACCTACA AGCCTCTAG	3337
TTCTGAAAAG TTGGAAGGGC ATCATGACCT CTTGGCCTCT CCTTTGATTC TCAATCTTC	3397
CCCAAAGCAT GGTTGGTGC CAGCCCCCTTC ACCTCCTTCC AGAGCCCAAG ATCAATGCTC	3457
AAGTTTGGA GGACATGATC ACCATCCCCA TGGTACTGAT GCTTGCTGGA TTTAGGGAGG	3517
GCATTTGCT ACCAAGCCTC TTCCCAACGC CCTGGGACCA GTCTTCTGTT TTGTTTTCA	3577
TTGTTTGAGC TTTCCACTGC ATGCCTTGAC TTCCCCCACC TCCTCCTCAA ACAAGAGACT	3637

CCACTGCATG TTCCAAGACA GTATGGGTG GTAAGATAAG GAAGGGAAGT GTGTGGATGT	3697
GGATGGTGGG GGCATGGACA AAGCTTGACA CATCAAGTTA TCAAGGCCTT GGAGGAGGCT	3757
CTGTATGTCC TCAGGGACT GACAACATCC TCCAGATTCC AGCCATAAAC CAATAACTAG	3817
GCTGGACCCCT TCCCAC TACA TAATAGGGCT CAGCCAGGCA GCCAGCTTG GGCTGAGCTA	3877
ACAGGACCAA TGGATTAAC T GGCATTCAG TCCAAGGAAG CTCGAAGCAG GTTTAGGACC	3937
AGGTCCCCTT GAGAGGTCAG AGGGGCCTCT GTGGGTGCTG GGTACTCCAG AGGTGCCACT	3997
GGTGGAAAGGG TCAGCGGAGC CCCAGCAGGA AGGGTGGGCC AGCCAGGCCA TTCTTAGTCC	4057
CTGGGTTGGG GAGGCAGGGA GCTAGGGCAG GGACCAAATG AACAGAAAGT CTCAGCCCAG	4117
GATGGGGCTT CTTCAACAGG CCCCTGCCCT CCTGAAGCCT CAGTCCTTCA CCTTGCCAGG	4177
TGCCGTTCT CTTCCGTGAA GGCCACTGCC CAGGTCCCCA GTGCGCCCC TAGTGGCCAT	4237
AGCCTGGTTA AAGTTCCCCA GTGCCTCCTT GTGATAGACC TTCTTCTCCC ACCCCCCTCT	4297
GCCCCTGGGT CCCCGGCCAT CCAGCGGGC TGCCAGAGAA CCCCAGACCT GCCCTTACAG	4357
TAGTGTAGCG CCCCTCCCT CTTTCGGCTG GTGTAGAATA GCCAGTAGTG TAGTGGGTG	4417
TGCTTTTACG TGATGGCGGG TGGGCAGCGG GCGCGGGCGT CCGCGCAGCC GTCTGTCCTT	4477
GATCTGCCCG CGGCGGCCCG TGTGTGTTT TGTGCTGTGT CCAGCGCTAA GGCGACCCCC	4537
TCCCCCGTAC TGACTTCTCC TATAAGCGCT TCTCTCGCA TAGTCACGTA GCTCCCACCC	4597
CACCCCTTTC CTGTGTCTCA CGCAAGTTTT ATACTCTAAT ATTTATATGG CTTTTTTTCT	4657
TCGACAAAAA AATAATAAAA CGTTTCTCT GAAAAAAA AAAAAAAA	4705

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val	
1 5 10 15	
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val	
20 25 30	
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly	
35 40 45	
Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg	
50 55 60	

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
 65 70 75 80
 Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
 85 90 95
 Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
 100 105 110
 Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
 115 120 125
 Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
 130 135 140
 Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
 145 150 155 160
 Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
 165 170 175
 Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
 180 185 190
 Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro.
 195 200 205
 Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
 210 215 220
 Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
 225 230 235 240
 Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
 245 250 255
 Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
 260 265 270
 Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
 275 280 285
 Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
 290 295 300
 Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
 305 310 315 320
 Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
 325 330 335
 Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
 340 345 350
 Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
 355 360 365
 Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
 370 375 380

Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
 385 390 395 400
 Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
 405 410 415
 Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
 420 425 430
 Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
 435 440 445
 Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
 450 455 460
 Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
 465 470 475 480
 Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
 485 490 495
 Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
 500 505 510
 Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
 515 520 525
 Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
 530 535 540
 Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
 545 550 555 560
 Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
 565 570 575
 Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
 580 585 590
 Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
 595 600 605
 Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
 610 615 620
 Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
 625 630 635 640
 Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
 645 650 655
 Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
 660 665 670
 Arg Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn
 675 680 685
 Leu Thr Phe Tyr Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe
 690 695 700

Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
 705 710 715 720
 Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
 725 730 735
 Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
 740 745 750
 Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
 755 760 765
 Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
 770 775 780
 Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
 785 790 795 800
 Gly Ala Glu Ser Ala Pro Pro Gly Gln Gln Ala Pro Pro Asn Thr Asp
 805 810 815
 Trp Arg Phe Ser Gln Ala Gln Arg Pro Gly Thr Ser Gly Ser Gln Asn
 820 825 830
 Gly Asp Asp Thr Gly Thr Trp Pro Asn Asn Gln Phe Asp Thr Glu Met
 835 840 845
 Leu Gln Ala Met Ile Leu Ala Ser Ala Ser Glu Ala Ala Asp Gly Ser
 850 855 860
 Ser Thr Leu Gly Gly Ala Gly Thr Met Gly Leu Ser Ala Arg Tyr
 865 870 875 880
 Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp Tyr Arg Gln Asn Val
 885 890 895
 Tyr Ile Pro Gly Ser Asn Ala His
 900

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 556 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Asp Trp Val Ile Pro Pro Ile Asn Leu Pro Glu Asn Ser Arg Gly Pro
 1 5 10 15
 Phe Pro Gln Glu Leu Val Arg Ile Arg Ser Asp Arg Asp Lys Asn Leu
 20 25 30

Ser Leu Arg Tyr Thr Val Thr Gly Pro Gly Ala Asp Gln Pro Pro Thr
 35 40 45
 Gly Ile Phe Ile Ile Asn Pro Ile Ser Gly Gln Leu Ser Val Thr Lys
 50 55 60
 Pro Leu Asp Arg Glu Gln Ile Ala Arg Phe His Leu Arg Ala His Ala
 65 70 75 80
 Val Asp Ile Asn Gly Asn Gln Val Glu Asn Pro Ile Asp Ile Val Ile
 85 90 95
 Asn Val Ile Asp Met Asn Asp Asn Arg Pro Glu Phe Leu His Gln Val
 100 105 110
 Trp Asn Gly Ser Val Pro Glu Gly Ser Lys Pro Gly Thr Tyr Val Met
 115 120 125
 Thr Val Thr Ala Ile Asp Ala Asp Asp Pro Asn Ala Leu Asn Gly Met
 130 135 140
 Leu Arg Tyr Arg Ile Leu Ser Gln Ala Pro Ser Thr Pro Ser Pro Asn
 145 150 155 160
 Met Phe Thr Ile Asn Asn Glu Thr Gly Asp Ile Ile Thr Val Ala Ala
 165 170 175
 Gly Leu Asp Arg Glu Lys Val Gln Gln Tyr Thr Leu Ile Ile Gln Ala
 180 185 190
 Thr Asp Met Glu Gly Asn Pro Thr Tyr Gly Leu Ser Asn Thr Ala Thr
 195 200 205
 Ala Val Ile Thr Val Thr Asp Val Asn Asp Asn Pro Pro Glu Phe Thr
 210 215 220
 Ala Met Thr Phe Tyr Gly Glu Val Pro Glu Asn Arg Val Asp Ile Ile
 225 230 235 240
 Val Ala Asn Leu Thr Val Thr Asp Lys Asp Gln Pro His Thr Pro Ala
 245 250 255
 Trp Asn Ala Val Tyr Arg Ile Ser Gly Gly Asp Pro Thr Gly Arg Phe
 260 265 270
 Ala Ile Gln Thr Asp Pro Asn Ser Asn Asp Gly Leu Val Thr Val Val
 275 280 285
 Lys Pro Ile Asp Phe Glu Thr Asn Arg Met Phe Val Leu Thr Val Ala
 290 295 300
 Ala Glu Asn Gln Val Pro Leu Ala Lys Gly Ile Gln His Pro Pro Gln
 305 310 315 320
 Ser Thr Ala Thr Val Ser Val Thr Val Ile Asp Val Asn Glu Asn Pro
 325 330 335
 Tyr Phe Ala Pro Asn Pro Lys Ile Ile Arg Gln Glu Glu Gly Leu His
 340 345 350

Ala Gly Thr Met Leu Thr Thr Phe Thr Ala Gly Asp Pro Asp Arg Tyr
 355 360 365
 Met Gln Gln Asn Ile Arg Tyr Thr Lys Leu Ser Asp Pro Ala Asn Trp
 370 375 380
 Leu Lys Ile Asp Pro Val Asn Gly Gln Ile Thr Thr Ile Ala Val Leu
 385 390 395 400
 Asp Arg Glu Ser Pro Asn Val Lys Asn Asn Ile Tyr Asn Ala Thr Phe
 405 410 415
 Leu Ala Ser Asp Asn Gly Ile Pro Pro Met Ser Gly Thr Gly Thr Leu
 420 425 430
 Gln Ile Tyr Leu Leu Asp Ile Asn Asp Asn Ala Pro Gln Val Leu Pro
 435 440 445
 Gln Glu Ala Glu Thr Cys Glu Thr Pro Asp Pro Asn Ser Ile Asn Ile
 450 455 460
 Thr Thr Ala Leu Asp Tyr Asp Ile Asp Pro Asn Ala Gly Pro Phe Ala
 465 470 475 480
 Phe Asp Leu Pro Leu Ser Pro Val Thr Ile Lys Arg Asn Trp Thr Ile
 485 490 495
 Thr Arg Leu Asn Gly Asp Phe Ala Gln Leu Asn Leu Lys Ile Lys Phe
 500 505 510
 Leu Glu Ala Gly Ile Tyr Glu Val Pro Ile Ile Ile Thr Asp Ser Gly
 515 520 525
 Asn Pro Pro Lys Ser Asn Lys Ser Ile Leu Arg Val Arg Val Cys Gln
 530 535 540
 Cys Asp Phe Asn Gly Asp Cys Thr Asp Val Asp Arg
 545 550 555

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Glu Asp Thr Val Tyr Ser Phe Asp Ile Pro Glu Asn Ala Gln Arg Gly
 1 5 10 15
 Tyr Gln Val Gly Gln Ile Val Ala Arg Asp Ala Asp Leu Gly Gln Asn
 20 25 30
 Ala Gln Leu Ser Tyr Gly Val Val Ser Asp Trp Ala Asn Asp Val Phe
 35 40 45

Ser	Leu	Asn	Pro	Gln	Thr	Gly	Met	Leu	Thr	Leu	Thr	Ala	Arg	Leu	Asp
50															
Tyr	Glu	Glu	Val	Gln	His	Tyr	Ile	Leu	Ile	Val	Gln	Ala	Gln	Asp	Asn
65															80
Gly	Gln	Pro	Ser	Leu	Ser	Thr	Thr	Ile	Thr	Val	Tyr	Cys	Asn	Val	Leu
															95
Asp	Leu	Asn	Asp	Asn	Ala	Pro	Ile								
															105

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Asp	Xaa	Asp	Xaa	Gly	Xaa	Asn
1						5

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Ala	Xaa	Asp	Xaa	Gly	Xaa	Pro
1						5

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4650 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 495..4103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

CCTCTATTCTG ACATTCTCTT TGGATTGTT TGCTATAACT TGAAATTGG GATGTCACAA	60
ACGAAACTGT CATCTGTTTC CGCCAAACTG TGGTCTGCT AATCTCCCAG GCTGGCAGCA	120
TTGGAGACTT GCTGACTTCT TTCATCCCCC ACTCTTTCA CCTGAAATTC CTTTCCTGG	180
TTTGCTCTA AGTCCTATGC TTCAGTCAGG GGCCAACCAA ATCTCACTGC CTCCTTTTA	240
TCATGAAGCC TTTGATCACT GATAGTTCTT TTTATATCTT GAAAAATCAC CCTTCCCAGT	300
ACAGTTAATA TTTAGTATCT CTACTCATCT TGGCACTTAC TCACAGCTCC ATAATTCA	360
CGTTTCGTA CCTCTTCATG GTGATGGGA GCCCTTGGA GGTGGTGACT GTGCTTTATA	420
CTCCTCATGA TGCTTCACAT GTGGCAGGGCG TGGAGTGCCTT GGAGGCGGCC CTCCTGATT	480
TGGGGCCTCC CAGG ATG GAG CCC CTG AGG CAC AGC CCA GGC CCT GGG GGG	530
Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly	
1 5 10	
CAA CGG CTA CTG CTG CCC TCC ATG CTG CTA GCA CTG CTG CTC CTG CTG	578
Gln Arg Leu Leu Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu	
15 20 25	
GCT CCA TCC CCA GGC CAC GCC ACT CGG GTA GTG TAC AAG GTG CCG GAG	626
Ala Pro Ser Pro Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu	
30 35 40	
GAA CAG CCA CCC AAC ACC CTC ATT GGG AGC CTC GCA GCC GAC TAT GGT	674
Glu Gln Pro Pro Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly	
45 50 55 60	
TTT CCA GAT GTG GGG CAC CTG TAC AAG CTA GAG GTG GGT GCC CCG TAC	722
Phe Pro Asp Val Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr	
65 70 75	
CTT CGC GTG GAT GGC AAG ACA GGT GAC ATT TTC ACC ACC GAG ACC TCC	770
Leu Arg Val Asp Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser	
80 85 90	
ATC GAC CGT GAG GGG CTC CGT GAA TGC CAG AAC CAG CTC CCT GGT GAT	818
Ile Asp Arg Glu Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp	
95 100 105	
CCC TGC ATC CTG GAG TTT GAG GTA TCT ATC ACA GAC CTC GTG CAG AAT	866
Pro Cys Ile Leu Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn	
110 115 120	
GCG AGC CCC CGG CTG CTA GAG GGC CAG ATA GAA GTA CAA GAC ATC AAT	914
Ala Ser Pro Arg Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn	
125 130 135 140	
GAC AAC ACA CCC AAC TTC GCC TCA CCA GTC ATC ACT CTG GCC ATC CCT	962
Asp Asn Thr Pro Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro	
145 150 155	
GAG AAC ACC AAC ATC GGC TCA CTC TTC CCC ATC CCG CTG GCT TCA GAC	1010
Glu Asn Thr Asn Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp	
160 165 170	

CGT GAT GCT GGT CCC AAC GGT GTG GCA TCC TAT GAG CTG CAG GTG GCA Arg Asp Ala Gly Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala 175 180 185	1058
GAG GAC CAG GAG GAG AAG CAA CCA CAG CTC ATT GTG ATG GGC AAC CTG Glu Asp Gln Glu Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu 190 195 200	1106
GAC CGT GAG CGC TGG GAC TCC TAT GAC CTC ACC ATC AAG GTG CAG GAT Asp Arg Glu Arg Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp 205 210 215 220	1154
GGC GGC AGC CCC CCA CGC GCC ACG AGT GCC CTG CTG CGT GTC ACC GTG Gly Gly Ser Pro Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val 225 230 235	1202
CTT GAC ACC AAT GAC AAC GCC CCC AAG TTT GAG CGG CCC TCC TAT GAG Leu Asp Thr Asn Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu 240 245 250	1250
GCC GAA CTA TCT GAG AAT AGC CCC ATA GGC CAC TCG GTC ATC CAG GTG Ala Glu Leu Ser Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val 255 260 265	1298
AAG GCC AAT GAC TCA GAC CAA GGT GCC AAT GCA GAA ATC GAA TAC ACA Lys Ala Asn Asp Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr 270 275 280	1346
TTC CAC CAG GCG CCC GAA GTT GTG AGG CGT CTT CTT CGA CTG GAC AGG Phe His Gln Ala Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg 285 290 295 300	1394
AAC ACT GGA CTT ATC ACT GTT CAG GGC CCG GTG GAC CGT GAG GAC CTA Asn Thr Gly Leu Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu 305 310 315	1442
AGC ACC CTG CGC TTC TCA GTG CTT GCT AAG GAC CGA GGC ACC AAC CCC Ser Thr Leu Arg Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro 320 325 330	1490
AAG AGT GCC CGT GCC CAG GTG GTT GTG ACC GTG AAG GAC ATG AAT GAC Lys Ser Ala Arg Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp 335 340 345	1538
AAT GCC CCC ACC ATT GAG ATC CGG GGC ATA GGG CTA GTG ACT CAT CAA Asn Ala Pro Thr Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln 350 355 360	1586
GAT GGG ATG GCT AAC ATC TCA GAG GAT GTG GCA GAG GAG ACA GCT GTG Asp Gly Met Ala Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val 365 370 375 380	1634
GCC CTG GTG CAG GTG TCT GAC CGA GAT GAG GGA GAG AAT GCA GCT GTC Ala Leu Val Gln Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val 385 390 395	1682
ACC TGT GTG GTG GCA GGT GAT GTG CCC TTC CAG CTG CGC CAG GCC AGT Thr Cys Val Val Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser 400 405 410	1730

GAG ACA GGC AGT GAC AGC AAG AAG AAG TAT TTC CTG CAG ACT ACC ACC Glu Thr Gly Ser Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Thr 415 420 425	1778
CCG CTA GAC TAC GAG AAG GTC AAA GAC TAC ACC ATT GAG ATT GTG GCT Pro Leu Asp Tyr Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala 430 435 440	1826
GTG GAC TCT GGC AAC CCC CCA CTC TCC AGC ACT AAC TCC CTC AAG GTG Val Asp Ser Gly Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val 445 450 455 460	1874
CAG GTG GTG GAC GTC AAT GAC AAC GCA CCT GTC TTC ACT CAG AGT GTC Gln Val Val Asp Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val 465 470 475	1922
ACT GAG GTC GCC TTC CCG GAA AAC AAC AAG CCT GGT GAA GTG ATT GCT Thr Glu Val Ala Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala 480 485 490	1970
GAG ATC ACT GCC AGT GAT GCT GAC TCT GGC TCT AAT GCT GAG CTG GTT Glu Ile Thr Ala Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val 495 500 505	2018
TAC TCT CTG GAG CCT GAG CCG GCT GCT AAG GGC CTC TTC ACC ATC TCA Tyr Ser Leu Glu Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser 510 515 520	2066
CCC GAG ACT GGA GAG ATC CAG GTG AAG ACA TCT CTG GAT CGG GAA CAG Pro Glu Thr Gly Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln 525 530 535 540	2114
CGG GAG AGC TAT GAG TTG AAG GTG GTG GCA GCT GAC CGG GGC AGT CCT Arg Glu Ser Tyr Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro 545 550 555	2162
AGC CTC CAG GGC ACA GCC ACT GTC CTT GTC AAT GTG CTG GAC TGC AAT Ser Leu Gln Gly Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn 560 565 570	2210
GAC AAT GAC CCC AAA TTT ATG CTG AGT GGC TAC AAC TTC TCA GTG ATG Asp Asn Asp Pro Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met 575 580 585	2258
GAG AAC ATG CCA GCA CTG AGT CCA GTG GGC ATG GTG ACT GTC ATT GAT Glu Asn Met Pro Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp 590 595 600	2306
GGA GAC AAG GGG GAG AAT GCC CAG GTG CAG CTC TCA GTG GAG CAG GAC Gly Asp Lys Gly Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp 605 610 615 620	2354
AAC GGT GAC TTT GTT ATC CAG AAT GGC ACA GGC ACC ATC CTA TCC AGC Asn Gly Asp Phe Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser 625 630 635	2402
CTG AGC TTT GAT CGA GAG CAA CAA AGC ACC TAC ACC TTC CAG CTG AAG Leu Ser Phe Asp Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys 640 645 650	2450

GCA GTG GAT GGT GGC GTC CCA CCT CGC TCA GCT TAC GTT GGT GTC ACC Ala Val Asp Gly Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr 655	660	665	2498
ATC AAT GTG CTG GAC GAG AAT GAC AAC GCA CCC TAT ATC ACT ACT GCC CCT Ile Asn Val Leu Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro 670	675	680	2546
TCT AAC ACC TCT CAC AAG CTG CTG ACC CCC CAG ACA CGT CTT GGT GAG Ser Asn Thr Ser His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu 685	690	695	700
ACG GTC AGC CAG GTG GCA GCC GAG GAC TTT GAC TCT GGT GTC AAT GCC Thr Val Ser Gln Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala 705	710	715	2642
GAG CTG ATC TAC AGC ATT GCA GGT GGC AAC CCT TAT GGA CTC TTC CAG Glu Leu Ile Tyr Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln 720	725	730	2690
ATT GGG TCA CAT TCA GGT GCC ATC ACC CTG GAG AAG GAG ATT GAG CGG Ile Gly Ser His Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg 735	740	745	2738
CGC CAC CAT GGG CTA CAC CGC CTG GTG GTG AAG GTC AGT GAC CGC GGC Arg His His Gly Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly 750	755	760	2786
AAG CCC CCA CGC TAT GGC ACA GCC TTG GTC CAT CTT TAT GTC AAT GAG Lys Pro Pro Arg Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu 765	770	775	2834
ACT CTG GCC AAC CGC ACG CTG CTG GAG ACC CTC CTG GGC CAC AGC CTG Thr Leu Ala Asn Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu 785	790	795	2882
GAC ACG CCG CTG GAT ATT GAC ATT GCT GGG GAT CCA GAA TAT GAG CGC Asp Thr Pro Leu Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg 800	805	810	2930
TCC AAG CAG CGT GGC AAC ATT CTC TTT GGT GTG GTG GCT GGT GTG GTG Ser Lys Gln Arg Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val 815	820	825	2978
GCC GTG GCC TTG CTC ATC GCC CTG GCG GTT CTT GTG CGC TAC TGC AGA Ala Val Ala Leu Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg 830	835	840	3026
CAG CGG GAG GCC AAA AGT GGT TAC CAG GCT GGT AAG AAG GAG ACC AAG Gln Arg Glu Ala Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys 845	850	855	3074
GAC CTG TAT GCC CCC AAG CCC AGT GGC AAG GCC TCC AAG GGA AAC AAA Asp Leu Tyr Ala Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys 865	870	875	3122
AGC AAA GGC AAG AAG AGC AAG TCC CCA AAG CCC GTG AAG CCA GTG GAG Ser Lys Gly Lys Lys Ser Lys Pro Lys Pro Val Lys Pro Val Glu 880	885	890	3170

GAC GAG GAT GAG GCC GGG CTG CAG AAG TCC CTC AAG TTC AAC CTG ATG Asp Glu Asp Glu Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met 895 900 905	3218
AGC GAT GCC CCT GGG GAC AGT CCC CGC ATC CAC CTG CCC CTC AAC TAC Ser Asp Ala Pro Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr 910 915 920	3266
CCA CCA GGC AGC CCT GAC CTG CGC CGC CAC TAT CGC TCT AAC TCC CCA Pro Pro Gly Ser Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro 925 930 935 940	3314
CTG CCT TCC ATC CAG CTG CAG CCC CAG TCA CCC TCA GCC TCC AAG AAG Leu Pro Ser Ile Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys 945 950 955	3362
CAC CAG GTG GTA CAG GAC CTG CCA CCT GCA AAC ACA TTC GTG GGC ACC His Gln Val Val Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr 960 965 970	3410
GGG GAC ACC ACG TCC ACG GGC TCT GAG CAG TAC TCC GAC TAC AGC TAC Gly Asp Thr Thr Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr 975 980 985	3458
CGC ACC AAC CCC CCC AAA TAC CCC AGC AAG CAG TTA CCT CAC CGC CGC Arg Thr Asn Pro Pro Lys Tyr Pro Ser Lys Gln Leu Pro His Arg Arg 990 995 1000	3506
GTC ACC TTC TCG GCC ACC AGC CAG GCC CAG GAG CTG CAG GAC CCA TCC Val Thr Phe Ser Ala Thr Ser Gln Ala Gln Glu Leu Gln Asp Pro Ser 1005 1010 1015 1020	3554
CAG CAC AGT TAC TAT GAC AGT GGC CTG GAG GAG TCT GAG ACG CCG TCC Gln His Ser Tyr Tyr Asp Ser Gly Leu Glu Glu Ser Glu Thr Pro Ser 1025 1030 1035	3602
AGC AAG TCA TCC TCA GGG CCT CGA CTC GGT CCC CTG GCC CTG CCT GAG Ser Lys Ser Ser Gly Pro Arg Leu Gly Pro Leu Ala Leu Pro Glu 1040 1045 1050	3650
GAT CAC TAT GAG CGC ACC ACC CCT GAT GGC AGC ATA GGA GAG ATG GAG Asp His Tyr Glu Arg Thr Pro Asp Gly Ser Ile Gly Glu Met Glu 1055 1060 1065	3698
CAC CCC GAG AAT GAC CTT CGC CCT TTG CCT GAT GTC GCC ATG ACA GGC His Pro Glu Asn Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly 1070 1075 1080	3746
ACA TGT ACC CGG GAG TGC AGT GAG TTT GGC CAC TCT GAC ACA TGC TGG Thr Cys Thr Arg Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp 1085 1090 1095 1100	3794
ATG CCT GGC CAG TCA TCT CCC AGC CGC CGG ACC AAG AGC AGC GCC CTC Met Pro Gly Gln Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu 1105 1110 1115	3842
AAA CTC TCC ACC TTC ATG CCT TAC CAG GAC CGA GGA GGG CAG GAG CCT Lys Leu Ser Thr Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro 1120 1125 1130	3890

GCG GGC GCC GGC AGC CCC AGC CCC CCG GAA GAC CGG AAC ACC AAA ACG Ala Gly Ala Gly Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr 1135 1140 1145	3938
GCC CCC GTG CGC CTC CTG CCC TCC TAC AGT GCC TTC TCC CAC AGT AGC Ala Pro Val Arg Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser 1150 1155 1160	3986
CAT GAT TCC TGC AAG GAC TCG GCC ACC TTG GAG GAA ATC CCC CTG ACC His Asp Ser Cys Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr 1165 1170 1175 1180	4034
CAG ACC TCG GAC TTC CCA CCC GCA GCC ACA CCG GCA TCT GCC CAG ACG Gln Thr Ser Asp Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr 1185 1190 1195	4082
GCC AAG CGC GAG ATC TAC CTG TGAGCCCCCT ACTGGCCGGC CCCCCCTCCCC Ala Lys Arg Glu Ile Tyr Leu 1200	4133
CAGCGCCGGC CAGCTCCCAA ATGCCCATTC CAGGGCCTCA CTCTCCACCC CTTCAGCGTG GACTTCCTGC CAGGGCCCAA GTGGGGGTAT CACTGACCTC ATGACCACGC TGGCCCTTCT	4193
CCCATGCAGG GTCCAGGTCC TCTCCCTCA TTTCCATCTC CCAGCCCAGG GGCCCCTTCC CCTTTATGGG GCTTCCCCCA GCTGATGCC AAGAGGGCTC CTCTGCAATG ACTGGGCTCC	4253
TTCCCTTGAC TTCCAGGGAG CACCCCTCG ATTTGGGCAG ATGGTGGAGT CAAGGGTGGG CAGCGTACTT CTAACTCATT GTTCCCTCA TGGCCGACCA GGGCGGGGAT AGCATGCCA	4313
ATTTTAGCCC TGAAGCAGGG CTGAACGGG GAGCCCCTTT CCCTGGGAGC TCCCAGAGGA AACTCTTGAC CACCAGTGGC TCCCTGAAGG GCTTTGTTA CCAAAGGTGG GGTAGGGACG	4373
GGGGTGGGAG TGGAGCGGAG GCCTTGTTT CCCGTGG 4493	4553
4613	4650

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1203 amino acids
 - (B) TYPE: amino acid
 - (C) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Met Glu Pro Leu Arg His Ser Pro Gly Pro Gly Gly Gln Arg Leu Leu 1 5 10 15
Leu Pro Ser Met Leu Leu Ala Leu Leu Leu Leu Ala Pro Ser Pro 20 25 30
Gly His Ala Thr Arg Val Val Tyr Lys Val Pro Glu Glu Gln Pro Pro 35 40 45

Asn Thr Leu Ile Gly Ser Leu Ala Ala Asp Tyr Gly Phe Pro Asp Val
 50 55 60

Gly His Leu Tyr Lys Leu Glu Val Gly Ala Pro Tyr Leu Arg Val Asp
 65 70 75 80

Gly Lys Thr Gly Asp Ile Phe Thr Thr Glu Thr Ser Ile Asp Arg Glu
 85 90 95

Gly Leu Arg Glu Cys Gln Asn Gln Leu Pro Gly Asp Pro Cys Ile Leu
 100 105 110

Glu Phe Glu Val Ser Ile Thr Asp Leu Val Gln Asn Ala Ser Pro Arg
 115 120 125

Leu Leu Glu Gly Gln Ile Glu Val Gln Asp Ile Asn Asp Asn Thr Pro
 130 135 140

Asn Phe Ala Ser Pro Val Ile Thr Leu Ala Ile Pro Glu Asn Thr Asn
 145 150 155 160

Ile Gly Ser Leu Phe Pro Ile Pro Leu Ala Ser Asp Arg Asp Ala Gly
 165 170 175

Pro Asn Gly Val Ala Ser Tyr Glu Leu Gln Val Ala Glu Asp Gln Glu
 180 185 190

Glu Lys Gln Pro Gln Leu Ile Val Met Gly Asn Leu Asp Arg Glu Arg
 195 200 205

Trp Asp Ser Tyr Asp Leu Thr Ile Lys Val Gln Asp Gly Gly Ser Pro
 210 215 220

Pro Arg Ala Thr Ser Ala Leu Leu Arg Val Thr Val Leu Asp Thr Asn
 225 230 235 240

Asp Asn Ala Pro Lys Phe Glu Arg Pro Ser Tyr Glu Ala Glu Leu Ser
 245 250 255

Glu Asn Ser Pro Ile Gly His Ser Val Ile Gln Val Lys Ala Asn Asp
 260 265 270

Ser Asp Gln Gly Ala Asn Ala Glu Ile Glu Tyr Thr Phe His Gln Ala
 275 280 285

Pro Glu Val Val Arg Arg Leu Leu Arg Leu Asp Arg Asn Thr Gly Leu
 290 295 300

Ile Thr Val Gln Gly Pro Val Asp Arg Glu Asp Leu Ser Thr Leu Arg
 305 310 315 320

Phe Ser Val Leu Ala Lys Asp Arg Gly Thr Asn Pro Lys Ser Ala Arg
 325 330 335

Ala Gln Val Val Val Thr Val Lys Asp Met Asn Asp Asn Ala Pro Thr
 340 345 350

Ile Glu Ile Arg Gly Ile Gly Leu Val Thr His Gln Asp Gly Met Ala
 355 360 365

Asn Ile Ser Glu Asp Val Ala Glu Glu Thr Ala Val Ala Leu Val Gln
 370 375 380
 Val Ser Asp Arg Asp Glu Gly Glu Asn Ala Ala Val Thr Cys Val Val
 385 390 395 400
 Ala Gly Asp Val Pro Phe Gln Leu Arg Gln Ala Ser Glu Thr Gly Ser
 405 410 415
 Asp Ser Lys Lys Lys Tyr Phe Leu Gln Thr Thr Pro Leu Asp Tyr
 420 425 430
 Glu Lys Val Lys Asp Tyr Thr Ile Glu Ile Val Ala Val Asp Ser Gly
 435 440 445
 Asn Pro Pro Leu Ser Ser Thr Asn Ser Leu Lys Val Gln Val Val Asp
 450 455 460
 Val Asn Asp Asn Ala Pro Val Phe Thr Gln Ser Val Thr Glu Val Ala
 465 470 475 480
 Phe Pro Glu Asn Asn Lys Pro Gly Glu Val Ile Ala Glu Ile Thr Ala
 485 490 495
 Ser Asp Ala Asp Ser Gly Ser Asn Ala Glu Leu Val Tyr Ser Leu Glu
 500 505 510
 Pro Glu Pro Ala Ala Lys Gly Leu Phe Thr Ile Ser Pro Glu Thr Gly
 515 520 525
 Glu Ile Gln Val Lys Thr Ser Leu Asp Arg Glu Gln Arg Glu Ser Tyr
 530 535 540
 Glu Leu Lys Val Val Ala Ala Asp Arg Gly Ser Pro Ser Leu Gln Gly
 545 550 555 560
 Thr Ala Thr Val Leu Val Asn Val Leu Asp Cys Asn Asp Asn Asp Pro
 565 570 575
 Lys Phe Met Leu Ser Gly Tyr Asn Phe Ser Val Met Glu Asn Met Pro
 580 585 590
 Ala Leu Ser Pro Val Gly Met Val Thr Val Ile Asp Gly Asp Lys Gly
 595 600 605
 Glu Asn Ala Gln Val Gln Leu Ser Val Glu Gln Asp Asn Gly Asp Phe
 610 615 620
 Val Ile Gln Asn Gly Thr Gly Thr Ile Leu Ser Ser Leu Ser Phe Asp
 625 630 635 640
 Arg Glu Gln Gln Ser Thr Tyr Thr Phe Gln Leu Lys Ala Val Asp Gly
 645 650 655
 Gly Val Pro Pro Arg Ser Ala Tyr Val Gly Val Thr Ile Asn Val Leu
 660 665 670
 Asp Glu Asn Asp Asn Ala Pro Tyr Ile Thr Ala Pro Ser Asn Thr Ser
 675 680 685

His Lys Leu Leu Thr Pro Gln Thr Arg Leu Gly Glu Thr Val Ser Gln
 690 695 700

Val Ala Ala Glu Asp Phe Asp Ser Gly Val Asn Ala Glu Leu Ile Tyr
 705 710 715 720

Ser Ile Ala Gly Gly Asn Pro Tyr Gly Leu Phe Gln Ile Gly Ser His
 725 730 735

Ser Gly Ala Ile Thr Leu Glu Lys Glu Ile Glu Arg Arg His His Gly
 740 745 750

Leu His Arg Leu Val Val Lys Val Ser Asp Arg Gly Lys Pro Pro Arg
 755 760 765

Tyr Gly Thr Ala Leu Val His Leu Tyr Val Asn Glu Thr Leu Ala Asn
 770 775 780

Arg Thr Leu Leu Glu Thr Leu Leu Gly His Ser Leu Asp Thr Pro Leu
 785 790 795 800

Asp Ile Asp Ile Ala Gly Asp Pro Glu Tyr Glu Arg Ser Lys Gln Arg
 805 810 815

Gly Asn Ile Leu Phe Gly Val Val Ala Gly Val Val Ala Val Ala Leu
 820 825 830

Leu Ile Ala Leu Ala Val Leu Val Arg Tyr Cys Arg Gln Arg Glu Ala
 835 840 845

Lys Ser Gly Tyr Gln Ala Gly Lys Lys Glu Thr Lys Asp Leu Tyr Ala
 850 855 860

Pro Lys Pro Ser Gly Lys Ala Ser Lys Gly Asn Lys Ser Lys Gly Lys
 865 870 875 880

Lys Ser Lys Ser Pro Lys Pro Val Lys Pro Val Glu Asp Glu Asp Glu
 885 890 895

Ala Gly Leu Gln Lys Ser Leu Lys Phe Asn Leu Met Ser Asp Ala Pro
 900 905 910

Gly Asp Ser Pro Arg Ile His Leu Pro Leu Asn Tyr Pro Pro Gly Ser
 915 920 925

Pro Asp Leu Gly Arg His Tyr Arg Ser Asn Ser Pro Leu Pro Ser Ile
 930 935 940

Gln Leu Gln Pro Gln Ser Pro Ser Ala Ser Lys Lys His Gln Val Val
 945 950 955 960

Gln Asp Leu Pro Pro Ala Asn Thr Phe Val Gly Thr Gly Asp Thr Thr
 965 970 975

Ser Thr Gly Ser Glu Gln Tyr Ser Asp Tyr Ser Tyr Arg Thr Asn Pro
 980 985 990

Pro Lys Tyr Pro Ser Lys Gln Leu Pro His Arg Arg Val Thr Phe Ser
 995 1000 1005

Ala Thr Ser Gln Ala Gln Glu Leu Gln Asp Pro Ser Gln His Ser Tyr
 1010 1015 1020

Tyr Asp Ser Gly Leu Glu Glu Ser Glu Thr Pro Ser Ser Lys Ser Ser
 1025 1030 1035 1040

Ser Gly Pro Arg Leu Gly Pro Leu Ala Leu Pro Glu Asp His Tyr Glu
 1045 1050 1055

Arg Thr Thr Pro Asp Gly Ser Ile Gly Glu Met Glu His Pro Glu Asn
 1060 1065 1070

Asp Leu Arg Pro Leu Pro Asp Val Ala Met Thr Gly Thr Cys Thr Arg
 1075 1080 1085

Glu Cys Ser Glu Phe Gly His Ser Asp Thr Cys Trp Met Pro Gly Gln
 1090 1095 1100

Ser Ser Pro Ser Arg Arg Thr Lys Ser Ser Ala Leu Lys Leu Ser Thr
 1105 1110 1115 1120

Phe Met Pro Tyr Gln Asp Arg Gly Gly Gln Glu Pro Ala Gly Ala Gly
 1125 1130 1135

Ser Pro Ser Pro Pro Glu Asp Arg Asn Thr Lys Thr Ala Pro Val Arg
 1140 1145 1150

Leu Leu Pro Ser Tyr Ser Ala Phe Ser His Ser Ser His Asp Ser Cys
 1155 1160 1165

Lys Asp Ser Ala Thr Leu Glu Glu Ile Pro Leu Thr Gln Thr Ser Asp
 1170 1175 1180

Phe Pro Pro Ala Ala Thr Pro Ala Ser Ala Gln Thr Ala Lys Arg Glu
 1185 1190 1195 1200

Ile Tyr Leu

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2789 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 115..2622

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA	60
CGCAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG	117
Met	
	1

GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG	165
Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val	
5 10 15	
GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT	213
Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile	
20 25 30	
CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
35 40 45	
GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG	309
Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg	
50 55 60 65	
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG	357
Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg	
70 75 80	
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG	405
Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu	
85 90 95	
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG	453
Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu	
100 105 110	
AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC	501
Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn	
115 120 125	
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC	549
Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser	
130 135 140 145	
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT	597
Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp	
150 155 160	
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT	645
Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn	
165 170 175	
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC	693
Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr	
180 185 190	
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT	741
Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser	
195 200 205	
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC	789
Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser	
210 215 220 225	
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG	837
Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala	
230 235 240	

CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys 245	250	255	885
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu 260	265	270	933
GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala 275	280	285	981
GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290	295	300	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310	315	320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325	330	335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340	345	350	1173
GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val 355	360	365	1221
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu 370	375	380	1269
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser 390	395	400	1317
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu 405	410	415	1365
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr 420	425	430	1413
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile 435	440	445	1461
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Tyr Asp Val Tyr Ile 450	455	460	1509
		465	

GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA AAC CTA AGT GTC TGG Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp 470	475	480	1557	
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG Asp Pro Asp Ala Pro Gln Ala Arg Leu Ser Phe Phe Leu Leu Glu 485	490	495	1605	
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg 500	505	510	1653	
GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg 515	520	525	1701	
CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val 530	535	540	545	1749
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp 550	555	560	1797	
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu 565	570	575	1845	
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val 580	585	590	1893	
GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595	600	605	1941	
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610	615	620	625	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630	635	640	2037	
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645	650	655	2085	
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660	665	670	2133	
GCC GAG TTC CCC TCT GGC TCT GCC CCC CGG GAG CAG AAA AAA AAT CTC Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn Leu 675	680	685	2181	
ACC TTT TAT CTA CTT CTT TCT CTA ATC CTG GTT TCT GTG GGC TTC GTG Thr Phe Tyr Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe Val 690	695	700	705	2229

GTC ACA GTG TTC GGA GTA ATC ATA TTC AAA GTT TAC AAG TGG AAG CAG	2277
Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys Gln	
710 715 720	
TCT AGA GAC CTA TAC CGA GCC CCG GTG AGC TCA CTG TAC CGA ACA CCA	2325
Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr Pro	
725 730 735	
GGG CCC TCC TTG CAC GCG GAC GCC GTG CGG GGA GGC CTG ATG TCG CCG	2373
Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser Pro	
740 745 750	
CAC CTT TAC CAT CAG GTG TAT CTC ACC ACG GAC TCC CGC CGC AGC GAC	2421
His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser Asp	
755 760 765	
CCG CTG CTG AAG AAA CCT GGT GCA GCC AGT CCA CTG GCC AGC CGC CAG	2469
Pro Leu Leu Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg Gln	
770 775 780 785	
AAC ACG CTG CGG AGC TGT GAT CCG GTG TTC TAT AGG CAG GTG TTG GGT	2517
Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu Gly	
790 795 800	
GCA GAG AGC GCC CCT CCC GGA CAG GTA AGG TTT AGC AAG TCA TGC TTG	2565
Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys Leu	
805 810 815	
ACC CTG TTA GTG CCT TTT TAT TCC TAC ATC ATA TTG AGA AGG CTG GAG	2613
Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu Glu	
820 825 830	
CTG TTT TTT TAGTGATGAA GATGTTTCC TGGTGATGCA TTCACACTTT	2662
Leu Phe Phe	
835	
CAACTGGCTC TTCCTAGATC AAAGTTAGTG CCTTTGTGAG ATGGTGGCCT GCCAGAGTGT	2722
GGTTTGTGGT CCCATTCAG GGGGAAGATA CTTGACTCAT CTGTGGACCT AATTCACATC	2782
CTCAGCG	2789

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 836 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val	
1 5 10 15	
Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val	
20 25 30	
Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly	
35 40 45	

Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg
 50 55 60

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
 65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
 85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
 100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
 115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
 130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
 145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
 165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
 180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
 195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
 210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
 225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
 245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
 260 265 270

Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
 275 280 285

Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
 290 295 300

Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
 305 310 315 320

Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
 325 330 335

Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
 340 345 350

Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
 355 360 365

Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
 370 375 380
 Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
 385 390 395 400
 Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
 405 410 415
 Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
 420 425 430
 Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
 435 440 445
 Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
 450 455 460
 Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
 465 470 475 480
 Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
 485 490 495
 Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
 500 505 510
 Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
 515 520 525
 Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
 530 535 540
 Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
 545 550 555 560
 Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
 565 570 575
 Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
 580 585 590
 Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
 595 600 605
 Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
 610 615 620
 Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
 625 630 635 640
 Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
 645 650 655
 Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
 660 665 670
 Arg Ala Glu Phe Pro Ser Gly Ser Ala Pro Arg Glu Gln Lys Lys Asn
 675 680 685

Leu Thr Phe Tyr Leu Leu Leu Ser Leu Ile Leu Val Ser Val Gly Phe
 690 695 700
 Val Val Thr Val Phe Gly Val Ile Ile Phe Lys Val Tyr Lys Trp Lys
 705 710 715 720
 Gln Ser Arg Asp Leu Tyr Arg Ala Pro Val Ser Ser Leu Tyr Arg Thr
 725 730 735
 Pro Gly Pro Ser Leu His Ala Asp Ala Val Arg Gly Gly Leu Met Ser
 740 745 750
 Pro His Leu Tyr His Gln Val Tyr Leu Thr Thr Asp Ser Arg Arg Ser
 755 760 765
 Asp Pro Leu Leu Lys Lys Pro Gly Ala Ala Ser Pro Leu Ala Ser Arg
 770 775 780
 Gln Asn Thr Leu Arg Ser Cys Asp Pro Val Phe Tyr Arg Gln Val Leu
 785 790 795 800
 Gly Ala Glu Ser Ala Pro Pro Gly Gln Val Arg Phe Ser Lys Ser Cys
 805 810 815
 Leu Thr Leu Leu Val Pro Phe Tyr Ser Tyr Ile Ile Leu Arg Arg Leu
 820 825 830
 Glu Leu Phe Phe
 835

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 115..2160

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CGAAAGCCAT GTCGGACTCG TCGCCCAGCG CCCAAGCGCT AACCCGCTGA AAGTTTCTCA 60
 GCGAAATCTC AGGGACGATC TGGACCCCGC TGAGAGGAAC TGCTTTGAG TGAG ATG 117
 Met
 1
 GTC CCA GAG GCC TGG AGG AGC GGA CTG GTA AGC ACC GGG AGG GTA GTG 165
 Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val Val
 5 10 15
 GGA GTT TTG CTT CTG CTT GGT GCC TTG AAC AAG GCT TCC ACG GTC ATT 213
 Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val Ile
 20 25 30

CAC TAT GAG ATC CCG GAG GAA AGA GAG AAG GGT TTC GCT GTG GGC AAC	261
His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly Asn	
35 40 45	
GTG GTC GCG AAC CTT GGT TTG GAT CTC GGT AGC CTC TCA GCC CGC AGG	309
Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg Arg	
50 55 60 65	
TTC CCG GTG GTG TCT GGA GCT AGC CGA AGA TTC TTT GAG GTG AAC CGG	357
Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn Arg	
70 75 80	
GAG ACC GGA GAG ATG TTT GTG AAC GAC CGT CTG GAT CGA GAG GAG CTG	405
Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu Leu	
85 90 95	
TGT GGG ACA CTG CCC TCT TGC ACT GTA ACT CTG GAG TTG GTA GTG GAG	453
Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val Glu	
100 105 110	
AAC CCG CTG GAG CTG TTC AGC GTG GAA GTG GTG ATC CAG GAC ATC AAC	501
Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile Asn	
115 120 125	
GAC AAC AAT CCT GCT TTC CCT ACC CAG GAA ATG AAA TTG GAG ATT AGC	549
Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile Ser	
130 135 140 145	
GAG GCC GTG GCT CCG GGG ACG CGC TTT CCG CTC GAG AGC GCG CAC GAT	597
Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His Asp	
150 155 160	
CCC GAT CTG GGA AGC AAC TCT TTA CAA ACC TAT GAG CTG AGC CGA AAT	645
Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg Asn	
165 170 175	
GAA TAC TTT GCG CTT CGC GTG CAG ACG CGG GAG GAC AGC ACC AAG TAC	693
Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys Tyr	
180 185 190	
GCG GAG CTG GTG TTG GAG CGC GCC CTG GAC CGA GAA CGG GAG CCT AGT	741
Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro Ser	
195 200 205	
CTC CAG TTA GTG CTG ACG GCG TTG GAC GGA GGG ACC CCA GCT CTC TCC	789
Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu Ser	
210 215 220 225	
GCC AGC CTG CCT ATT CAC ATC AAG GTG CTG GAC GCG AAT GAC AAT GCG	837
Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn Ala	
230 235 240	
CCT GTC TTC AAC CAG TCC TTG TAC CGG GCG CGC GTT CCT GGA GGA TGC	885
Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly Cys	
245 250 255	
ACC TCC GGC ACG CGC GTG GTA CAA GTC CTT GCA ACG GAT CTG GAT GAA	933
Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp Glu	
260 265 270	

GGC CCC AAC GGT GAA ATT ATT TAC TCC TTC GGC AGC CAC AAC CGC GCC Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg Ala 275 280 285	981
GGC GTG CGG CAA CTA TTC GCC TTA GAC CTT GTA ACC GGG ATG CTG ACA Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu Thr 290 295 300 305	1029
ATC AAG GGT CGG CTG GAC TTC GAG GAC ACC AAA CTC CAT GAG ATT TAC Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile Tyr 310 315 320	1077
ATC CAG GCC AAA GAC AAG GGC GCC AAT CCC GAA GGA GCA CAT TGC AAA Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys Lys 325 330 335	1125
GTG TTG GTG GAG GTT GTG GAT GTG AAT GAC AAC GCC CCG GAG ATC ACA Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile Thr 340 345 350	1173
GTC ACC TCC GTG TAC AGC CCA GTA CCC GAG GAT GCC TCT GGG ACT GTC Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr Val 355 360 365	1221
ATC GCT TTG CTC AGT GTG ACT GAC CTG GAT GCT GGC GAG AAC GGG CTG Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly Leu 370 375 380 385	1269
GTG ACC TGC GAA GTT CCA CCG GGT CTC CCT TTC AGC CTT ACT TCT TCC Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser Ser 390 395 400	1317
CTC AAG AAT TAC TTC ACT TTG AAA ACC AGT GCA GAC CTG GAT CGG GAG Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg Glu 405 410 415	1365
ACT GTG CCA GAA TAC AAC CTC AGC ATC ACC GCC CGA GAC GCC GGA ACC Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly Thr 420 425 430	1413
CCT TCC CTC TCA GCC CTT ACA ATA GTG CGT GTT CAA GTG TCC GAC ATC Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp Ile 435 440 445	1461
AAT GAC AAC CCT CCA CAA TCT TCT CAA TCT TCC TAC GAC GTT TAC ATT Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr Ile 450 455 460 465	1509
GAA GAA AAC AAC CTC CCC GGG GCT CCA ATA CTA AAC CTA AGT GTC TGG Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val Trp 470 475 480	1557
GAC CCC GAC GCC CCG CAG AAT GCT CGG CTT TCT TTC TTT CTC TTG GAG Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu Glu 485 490 495	1605
CAA GGA GCT GAA ACC GGG CTA GTG GGT CGC TAT TTC ACA ATA AAT CGT Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn Arg 500 505 510	1653

GAC AAT GGC ATA GTG TCA TCC TTA GTG CCC CTA GAC TAT GAG GAT CGG Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp Arg 515	520	525	1701
CGG GAA TTT GAA TTA ACA GCT CAT ATC AGC GAT GGG GGC ACC CCG GTC Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro Val 530	535	540	1749
CTA GCC ACC AAC ATC AGC GTG AAC ATA TTT GTC ACT GAT CGC AAT GAC Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn Asp 550	555	560	1797
AAT GCC CCC CAG GTC CTA TAT CCT CGG CCA GGT GGG AGC TCG GTG GAG Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val Glu 565	570	575	1845
ATG CTG CCT CGA GGT ACC TCA GCT GGC CAC CTA GTG TCA CGG GTG GTA Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val Val 580	585	590	1893
GGC TGG GAC GCG GAT GCA GGG CAC AAT GCC TGG CTC TCC TAC AGT CTC Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser Leu 595	600	605	1941
TTT GGA TCC CCT AAC CAG AGC CTT TTT GCC ATA GGG CTG CAC ACT GGT Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr Gly 610	615	620	1989
CAA ATC AGT ACT GCC CGT CCA GTC CAA GAC ACA GAT TCA CCC AGG CAG Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg Gln 630	635	640	2037
ACT CTC ACT GTC TTG ATC AAA GAC AAT GGG GAG CCT TCG CTC TCC ACC Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser Thr 645	650	655	2085
ACT GCT ACC CTC ACT GTG TCA GTA ACC GAG GAC TCT CCT GAA GCC CGA Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala Arg 660	665	670	2133
GCC GAG TTC CCC TCT GGC TCT GCC AGT TAAACCTTCT TTAATTATGG Ala Glu Phe Pro Ser Gly Ser Ala Ser 675	680		2180
ATTAGCCATT AACATTTTG AAACGTGGAC CATTAAACCT CGGCCTACCC CCTCCAAC TG			2240
TCCTGGTGAT GAGTCATTA GCTAAGTTAA ATTAATTGAA CTTTGATCTA AACCAAAACA			2300
AATCAGGAAA ATAAAGCTGT AAAGGAACCTT ATCAAGCATT CCAAAACCAA CTAGAAATTAA			2360
CTTGAAGTTT CGAGTGAGCA TTGCCTGTGC CAGTATTCTT CATTATAGGA TTATAAATC			2420
GTTTTTTTCC CAAAGCGCAT GTCTACGCCA GGCAGAGGAG TAATTATTCA GCCAATTCA			2480
TGGATGTAAC GATGGATATA AATAATTGAT AGCACCTAGA GGCTTCCAGT TTGGGTGGAA			2540
GGCTAAAAGT AGAGGGGAAC TCACTCACTT GAGAAATGAT ATTTAAGTGA ATAAATAGTT			2600
CTCTTCTATG AAACTATTAC TATTTAGTTC TCTGGAAAAC TTAAGTGTAT TAATGATTAG			2660
AACATCAAAT CCTAAGTAAA GAAATGACAT TTTAAATATA AAAAGCCAAA CTTTAAATAA			2720

ATCATAGAGA CCTCAGACAT AATATAGGAA A

2751

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 682 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Pro Glu Ala Trp Arg Ser Gly Leu Val Ser Thr Gly Arg Val
 1 5 10 15

Val Gly Val Leu Leu Leu Gly Ala Leu Asn Lys Ala Ser Thr Val
 20 25 30

Ile His Tyr Glu Ile Pro Glu Glu Arg Glu Lys Gly Phe Ala Val Gly
 35 40 45

Asn Val Val Ala Asn Leu Gly Leu Asp Leu Gly Ser Leu Ser Ala Arg
 50 55 60

Arg Phe Pro Val Val Ser Gly Ala Ser Arg Arg Phe Phe Glu Val Asn
 65 70 75 80

Arg Glu Thr Gly Glu Met Phe Val Asn Asp Arg Leu Asp Arg Glu Glu
 85 90 95

Leu Cys Gly Thr Leu Pro Ser Cys Thr Val Thr Leu Glu Leu Val Val
 100 105 110

Glu Asn Pro Leu Glu Leu Phe Ser Val Glu Val Val Ile Gln Asp Ile
 115 120 125

Asn Asp Asn Asn Pro Ala Phe Pro Thr Gln Glu Met Lys Leu Glu Ile
 130 135 140

Ser Glu Ala Val Ala Pro Gly Thr Arg Phe Pro Leu Glu Ser Ala His
 145 150 155 160

Asp Pro Asp Leu Gly Ser Asn Ser Leu Gln Thr Tyr Glu Leu Ser Arg
 165 170 175

Asn Glu Tyr Phe Ala Leu Arg Val Gln Thr Arg Glu Asp Ser Thr Lys
 180 185 190

Tyr Ala Glu Leu Val Leu Glu Arg Ala Leu Asp Arg Glu Arg Glu Pro
 195 200 205

Ser Leu Gln Leu Val Leu Thr Ala Leu Asp Gly Gly Thr Pro Ala Leu
 210 215 220

Ser Ala Ser Leu Pro Ile His Ile Lys Val Leu Asp Ala Asn Asp Asn
 225 230 235 240

Ala Pro Val Phe Asn Gln Ser Leu Tyr Arg Ala Arg Val Pro Gly Gly
 245 250 255

Cys Thr Ser Gly Thr Arg Val Val Gln Val Leu Ala Thr Asp Leu Asp
 260 265 270
 Glu Gly Pro Asn Gly Glu Ile Ile Tyr Ser Phe Gly Ser His Asn Arg
 275 280 285
 Ala Gly Val Arg Gln Leu Phe Ala Leu Asp Leu Val Thr Gly Met Leu
 290 295 300
 Thr Ile Lys Gly Arg Leu Asp Phe Glu Asp Thr Lys Leu His Glu Ile
 305 310 315 320
 Tyr Ile Gln Ala Lys Asp Lys Gly Ala Asn Pro Glu Gly Ala His Cys
 325 330 335
 Lys Val Leu Val Glu Val Val Asp Val Asn Asp Asn Ala Pro Glu Ile
 340 345 350
 Thr Val Thr Ser Val Tyr Ser Pro Val Pro Glu Asp Ala Ser Gly Thr
 355 360 365
 Val Ile Ala Leu Leu Ser Val Thr Asp Leu Asp Ala Gly Glu Asn Gly
 370 375 380
 Leu Val Thr Cys Glu Val Pro Pro Gly Leu Pro Phe Ser Leu Thr Ser
 385 390 395 400
 Ser Leu Lys Asn Tyr Phe Thr Leu Lys Thr Ser Ala Asp Leu Asp Arg
 405 410 415
 Glu Thr Val Pro Glu Tyr Asn Leu Ser Ile Thr Ala Arg Asp Ala Gly
 420 425 430
 Thr Pro Ser Leu Ser Ala Leu Thr Ile Val Arg Val Gln Val Ser Asp
 435 440 445
 Ile Asn Asp Asn Pro Pro Gln Ser Ser Gln Ser Ser Tyr Asp Val Tyr
 450 455 460
 Ile Glu Glu Asn Asn Leu Pro Gly Ala Pro Ile Leu Asn Leu Ser Val
 465 470 475 480
 Trp Asp Pro Asp Ala Pro Gln Asn Ala Arg Leu Ser Phe Phe Leu Leu
 485 490 495
 Glu Gln Gly Ala Glu Thr Gly Leu Val Gly Arg Tyr Phe Thr Ile Asn
 500 505 510
 Arg Asp Asn Gly Ile Val Ser Ser Leu Val Pro Leu Asp Tyr Glu Asp
 515 520 525
 Arg Arg Glu Phe Glu Leu Thr Ala His Ile Ser Asp Gly Gly Thr Pro
 530 535 540
 Val Leu Ala Thr Asn Ile Ser Val Asn Ile Phe Val Thr Asp Arg Asn
 545 550 555 560
 Asp Asn Ala Pro Gln Val Leu Tyr Pro Arg Pro Gly Gly Ser Ser Val
 565 570 575

Glu Met Leu Pro Arg Gly Thr Ser Ala Gly His Leu Val Ser Arg Val
 580 585 590
 Val Gly Trp Asp Ala Asp Ala Gly His Asn Ala Trp Leu Ser Tyr Ser
 595 600 605
 Leu Phe Gly Ser Pro Asn Gln Ser Leu Phe Ala Ile Gly Leu His Thr
 610 615 620
 Gly Gln Ile Ser Thr Ala Arg Pro Val Gln Asp Thr Asp Ser Pro Arg
 625 630 635 640
 Gln Thr Leu Thr Val Leu Ile Lys Asp Asn Gly Glu Pro Ser Leu Ser
 645 650 655
 Thr Thr Ala Thr Leu Thr Val Ser Val Thr Glu Asp Ser Pro Glu Ala
 660 665 670
 Arg Ala Glu Phe Pro Ser Gly Ser Ala Ser
 675 680

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2831 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCTGGCA CGAGGGCTGAA CTGAGGGTGA CGGACATAAA CGACTATTCT CCAGTGTCA	60
GTGAAAGAGA AATGATACTG AGGATACCAAG AAAACAGTGC TCGGGGAAAT ACATTCCCTT	120
TAAACAATGC TCTGGACTCA GACGTAGATA TCAACAATAT CCAGACCTAT AGGCTCAGCT	180
CAAACCTCTCA TTTCTGGTT GTAACCCGCA ACCGCAGTGA TGGCAGGAAG TACCCAGAGC	240
TGGTGCTGGA GAAAGAACTG GATCGAGAGG AGGAACCTGA GCTGAGGTTA ACGCTGACAG	300
CTTTGGATGG TGGCTCTCCT CCCCGGTCTG GGACGACACA GGTCCCTCATT GAAGTAGTGG	360
ACACCAACGA TAATGCACCC GAGTTTCAGC AGCCAACATA CCAAGTGCAA ACTCCCGAGA	420
ACAGTCCCAC CGGCTCTCTG GTACTCACAG TCTCAGCCAA TGACTTAGAC AGTGGAGACT	480
ATGGGAAAGT CTTGTACGCA CTTTCGCAAC CCTCAGAAGA TATTAGCAAA ACATTCGAGG	540
TAAACCCCTGT AACCGGGGAA ATTGCCTAC GAAAAGAGGT GAATTTGAA ACTATTCCCTT	600
CGTATGAAGT GGTTATCAAG GGGACGGACG GGGGAGGTCT CTCAGGAAAA TGCACCTCTGT	660
TACTGCAGGT GGTGGACGTG AATGACAATG CCCCAGAAGT GATGCTATCT GCGCTAACCA	720
ACCCAGTCCC AGAAAATTCC CCCGATGAGG TAGTGGCTGT TTTCAGTGTT AGAGATCCTG	780
ACTCTGGGAA CAACGGAAAA GTGATTGCAT CCATCGAGGA AGACCTGCC 840	TTTCTTCTAA

AATCTTCAGG AAAGAACTTT TACACTTTAG TAACCAAGGG AGCACTTGAC AGGGAAGAAA	900
GAGAGCAATT GAACATCACC ATCACAGTCA CTGACCTGGG CATAACCCAGG CTCACCACCC	960
AACACACCAT AACAGTGCAG GTGGCAGACA TCAACGACAA TGCCCCCTCC TTCACCCAAA	1020
CCTCCTACAC CATGTTTGTCA CGCGAGAACCA ACAGCCCCGC CCTGCACATA GGCACCATCA	1080
GCGCCACAGA CTCAGACTCA GGATCCAATG CCCACATCAC CTACTCGCTG CTACCGCCCC	1140
AAGACCCACA GCTGGCCCTC GACTCGCTCA TCTCCATCAA TGTAGACAAAC GGGCAGCTGT	1200
TCGCGCTCAG GGCCTAGAC TATGAGGCTC TGCAGGGCTT CGAGTTCCAT GTGGGCGCCA	1260
CAGACCAAGG CTCGCCCGCG CTCAGCAGCC AGGCTCTGGT GCACGTGGTG GTGTTGGACG	1320
ACAATGACAA TGCGCCCTTC GTGCTCTACC CGCTGAAAAA CGCCTCTGCA CCCTTCACTG	1380
AGCTGCTGCC CAGGGCGGCA GAGCCTGGAT ACCTGGTTAC CAAGGTGGTA GCTGTGGACC	1440
GCGACTCTGG CCAGAATGCC TGGCTGTCAT TCCAGCTGCT CAAGGCCACG GAGCCCGGGC	1500
TGTTCAACGT ATGGGCGCAC AATGGCGAGG TACGCACCTC CAGGCTGCTG AGCGAGCGCG	1560
ACGCACCCAA GCACAAGCTG CTGCTGTTGG TCAAGGACAA TGGAGATCCT CCACGCTCTG	1620
CCAGTGTAC TCTGCACGTG CTAGTGGTGG ATGCCCTCTC TCAGCCCTAC CTGCCTCTGC	1680
CAGAGGTGGC GCACGACCCCT GCACAAGAACG AAGATGCGCT AACACTCTAC CTGGTCATAG	1740
CTTTGGCATC TGTGTCTTCT CTCTTCCTCT TGTCTGTGCT GCTGTTCGTG GGGGTGAGGC	1800
TCTGCAGGAG GGCCAGGGCA GCCTCTCTGA GTGCCTATTG TGTGCCTGAA GGCCACTTTTC	1860
CTGGCCAGCT GGTGGATGTC AGAGGTATGG GGACCCCTGTC CCAGAGCTAC CAGTATGATG	1920
TATGTCTGAT GGGGGATTCT TCTGGGACCA GCGAATTAA CTTCTTAAAG CCAGTTCTGC	1980
CTAGCTCTCT GCACCAGTGC TCTGGAAAG AAATAGAGGA AAATTCCACA CTCCAGAATA	2040
GTCCCCGGTT TCATCATTAA TAGAAAAGTA CTTTACAGAT ATTTAATTCC AAATATCATC	2100
TTGTTGATTA ACTAAAGTCT GTTCACATGT AGCTAGCTAG CAACGATTTT AATGTTCACT	2160
TTACCCATCT TTTTCAGGG TCATGTCTAA AGCTACAAGT TTGNCTTTAC TTATACCTGT	2220
CGCACAGAAAT NNNNNNNNNN TGGGTATAA GTCACAGTCA TGGGATACTG GCACAAGATG	2280
GCAGCTTGAT TGCTCAGTTA TGGCTGCAA GGGGNGCTTG AGTTTAGGGA ATGTGTTAGA	2340
GCTGGAATAA GTTTCTGAG AAATGTGTAA GACAAATTTC TTTTGCACAT TCCCTGTGTT	2400
CCTGTACCCC TGTTCCAGA ACTACGAAAT GTGTCATCAG AAGGCATGCT CACATTTCC	2460
CCTTTGTTG CGTGACCCGG GTGCCAGAAA TTAAATAAAA TTAGCATGGA GTTCAATGCA	2520
GCATTAAAAC AAAGTTACTT CTACAAACCT TTTATTGAC GGTTAAAATT GTAACCTCCC	2580
CACCCATGAG GCTGGCTGTA AGAACCAAGTA TGAATGGGTG TCTATCGCAA CCTTATTTC	2640
AAAAATCAAA CAAAAGGAGA AATGAGAGAC CAAACAAACAC GCTACAGGAA AGATTCATA	2700

AGGATGTATG TATGGACACA AAAACTGGGA TACAGACATT TTAAATCTGT TGGTACCACA	2760
TGGTGGCGCT GCAGGCTAAA GAAATGCAAG GGAAATTAAA AAGAGGCTGA GCTAGAAGTC	2820
AAAAAAAAAA A	2831

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3353 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 763..3123

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GTATTTTCC ACAGTTAAA ATTTCATAA AATCATACT CTCTGACTTT ATGTAGAAAG	60
GATACCACAC TGGAATTAAC GTGTAGCTTT TTCTTGATGT AATCCAACCA ATGGGAGCAC	120
AATTCTGGTA CATAGGCTGT CTAGAATTG AAAGAAATTAA AAGAATTCA TTTGTTTGCG	180
TGATAAATT TTAAAGAAATC ACGTGGCTTT ATGTTATTAT TATTACAAGA TGACTGATCA	240
CTATTATGTC TTCTTCACT TCTCAATTTC CCTCAGAACCA CTACACCCAG ACTACAGGCT	300
CTGGAGGGTG GGGACCATGT CTGGGTTGTT TACTGATGTA TTTCATAATT TGGCACATAG	360
AGACCAATAA TACTCCTTTA AATGAAGAAA TTAATAATTAA CCATTGCGTG ATATTGTGAT	420
TACATCATTT CCTCCCAATT TCCAACTCC TAATAGAATA GAGAATAGAT CAATTGTAGC	480
AATTCTGTTA GAAGCAAAGA CAACGCATGG TGGCGCTGCA GGCTAAGGCT TCAAAAAAAG	540
GAAAAGGAAA AAGCCCATGA AATGCTACTA GCTACTTCAG ACCTCTTCA GCCTAAGAGG	600
AAAGCCTGTT AGCAGAGCAC GGACCAGTGT CTCCGGAGAA TGCTATTCTC CTACATTCC	660
GAACAGGTTA TCAACGCACA GATCGATCAC TGCCTCTGTC CCATCGCTCC CTGAAGTAGC	720
TCTGACTCCG GTTCCTTGAA AGGGCGTGT ACAGAAGTAA AG ATG GAG CCT GCA	774
Met Glu Pro Ala	
1	
GGG GAG CGC TTT CCC GAA CAA AGG CAA GTC CTG ATT CTC CTT CTT TTA	822
Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile Leu Leu Leu	
5 10 15 20	
CTG GAA GTG ACT CTG GCA GGC TGG GAA CCC CGT CGC TAT TCT GTG ATG	870
Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg Tyr Ser Val Met	
25 30 35	

GAG GAA ACA GAG AGA GGT TCT TTT GTA GCC AAC CTG GCC AAT GAC CTA Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu Ala Asn Asp Leu 40	45	50	918
GGG CTG GGA GTG GGG GAG CTA GCC GAG CGG GGA GCC CGG GTA GTT TCT Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala Arg Val Val Ser 55	60	65	966
GAG GAT AAC GAA CAA GGC TTG CAG CTT GAT CTG CAG ACC GGG CAG TTG Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln Thr Gly Gln Leu 70	75	80	1014
ATA TTA AAT GAG AAG CTG GAC CGG GAG AAG CTG TGT GGC CCT ACT GAG Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys Gly Pro Thr Glu 85	90	95	1062
CCC TGT ATA ATG CAT TTC CAA GTG TTA CTG AAA AAA CCT TTG GAA GTA Pro Cys Ile Met His Phe Gln Val Leu Lys Lys Pro Leu Glu Val 105	110	115	1110
TTT CGA GCT GAA CTA CTA GTG ACA GAC ATA AAC GAT CAT TCT CCT GAG Phe Arg Ala Glu Leu Leu Val Thr Asp Ile Asn Asp His Ser Pro Glu 120	125	130	1158
TTT CCT GAA AGA GAA ATG ACC CTG AAA ATC CCA GAA ACT AGC TCC CTT Phe Pro Glu Arg Glu Met Thr Leu Lys Ile Pro Glu Thr Ser Ser Leu 135	140	145	1206
GGG ACT GTG TTT CCT CTG AAA AAA GCT CGG GAC TTG GAC GTG GGC AGC Gly Thr Val Phe Pro Leu Lys Ala Arg Asp Leu Asp Val Gly Ser 150	155	160	1254
AAT AAT GTT CAA AAC TAC AAT ATT TCT CCC AAT TCT CAT TTC CAT GTT Asn Asn Val Gln Asn Tyr Asn Ile Ser Pro Asn Ser His Phe His Val 165	170	175	1302
TCC ACT CGC ACC CGA GGG GAT GGC AGG AAA TAC CCA GAG CTG GTG CTG Ser Thr Arg Thr Arg Gly Asp Gly Arg Lys Tyr Pro Glu Leu Val Leu 185	190	195	1350
GAC ACA GAA CTG GAT CGC GAG GAG CAG GCC GAG CTC AGA TTA ACC TTG Asp Thr Glu Leu Asp Arg Glu Gln Ala Glu Leu Arg Leu Thr Leu 200	205	210	1398
ACA GCG GTG GAC GGT GGC TCT CCA CCC CGA TCT GGC ACC GTC CAG ATC Thr Ala Val Asp Gly Gly Ser Pro Pro Arg Ser Gly Thr Val Gln Ile 215	220	225	1446
CTC ATC TTG GTC TTG GAC GCC AAT GAC AAT GCC CCG GAG TTT GTG CAG Leu Ile Leu Val Asp Ala Asn Asp Asn Ala Pro Glu Phe Val Gln 230	235	240	1494
CGC CTC TAC GAG GTG CAG GTC CCA GAG AAC AGC CCA GTA GGC TCC CTA Ala Leu Tyr Glu Val Gln Val Pro Glu Asn Ser Pro Val Gly Ser Leu 245	250	255	1542
GTT GTC AAG GTC TCT GCT AGG GAT TTA GAC ACT GGG ACA AAT GGA GAG Val Val Lys Val Ser Ala Arg Asp Leu Asp Thr Gly Thr Asn Gly Glu 265	270	275	1590

ATA TCA TAC TCC CTT TAT TAC AGC TCT CAG GAG ATA GAC AAA CCT TTT Ile Ser Tyr Ser Leu Tyr Tyr Ser Ser Gln Glu Ile Asp Lys Pro Phe 280	285	290	1638
GAG CTA AGC AGC CTT TCA GGA GAA ATT CGA CTA ATT AAA AAA CTA GAT Glu Leu Ser Ser Leu Ser Gly Glu Ile Arg Leu Ile Lys Lys Leu Asp 295	300	305	1686
TTT GAG ACA ATG TCT TCA TAT GAT CTA GAT ATA GAG GCA TCT GAT GGC Phe Glu Thr Met Ser Ser Tyr Asp Leu Asp Ile Glu Ala Ser Asp Gly 310	315	320	1734
GGG GGA CTT TCT GGA AAA TGC TCT GTC TCT GTT AAG GTG CTG GAT GTT Gly Gly Leu Ser Gly Lys Cys Ser Val Ser Val Lys Val Leu Asp Val 325	330	335	1782
AAC GAT AAC TTC CCG GAA CTA AGT ATT TCA TCA CTT ACC AGC CCT ATT Asn Asp Asn Phe Pro Glu Leu Ser Ile Ser Ser Leu Thr Ser Pro Ile 345	350	355	1830
CCC GAG AAT TCT CCA GAG ACA GAA GTG GCC CTG TTT AGG ATT AGA GAC Pro Glu Asn Ser Pro Glu Thr Glu Val Ala Leu Phe Arg Ile Arg Asp 360	365	370	1878
CGA GAC TCT GGA GAA AAT GGA AAA ATG ATT TGC TCA ATT CAG GAT GAT Arg Asp Ser Gly Glu Asn Gly Lys Met Ile Cys Ser Ile Gln Asp Asp 375	380	385	1926
GTG CCT TTT AAG CTA AAA CCT TCT GTT GAG AAT TTC TAC AGG CTG GTA Val Pro Phe Lys Leu Lys Pro Ser Val Glu Asn Phe Tyr Arg Leu Val 390	395	400	1974
ACA GAA GGG GCG CTG GAC AGA GAG ACC AGA GCC GAG TAC AAC ATC ACC Thr Glu Gly Ala Leu Asp Arg Glu Thr Arg Ala Glu Tyr Asn Ile Thr 405	410	415	2022
ATC ACC ATC ACA GAC TTG GGG ACT CCA AGG CTG AAA ACC GAG CAG AGC Ile Thr Ile Thr Asp Leu Gly Thr Pro Arg Leu Lys Thr Glu Gln Ser 425	430	435	2070
ATA ACC GTG CTG GTG TCG GAC GTC AAT GAC AAC GCC CCC GCC TTC ACC Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala Pro Ala Phe Thr 440	445	450	2118
CAA ACC TCC TAC ACC CTG TTC GTC CGC GAG AAC AAC AGC CCC GCC CTG Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser Pro Ala Leu 455	460	465	2166
CAC ATC GGC AGT GTC AGC GCC ACA GAC AGA GAC TCG GGC ACC AAC GCC His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser Gly Thr Asn Ala 470	475	480	2214
CAG GTC ACC TAC TCG CTG CTG CCG CCC CAG GAC CCG CAC CTG CCC CTA Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp Pro His Leu Pro Leu 485	490	495	2262
ACC TCC CTG GTC TCC ATT AAC ACG GAC AAC GGC CAC CTG TTC GCT CTC Thr Ser Leu Val Ser Ile Asn Thr Asp Asn Gly His Leu Phe Ala Leu 505	510	515	2310

CAG TCG CTG GAC TAC GAG GCC CTG CAG GCT TTC GAG TTC CGC GTG GGC Gln Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe Glu Phe Arg Val Gly 520	525	530	2358
GCC ACA GAC CGC GGC TTC CCG GCG CTG AGC AGC GAG GCG CTG GTG CGA Ala Thr Asp Arg Gly Phe Pro Ala Leu Ser Ser Glu Ala Leu Val Arg 535	540	545	2406
GTG CTG GTG CTG GAC GCC AAC GAC AAC TCG CCC TTC GTG CTG TAC CCG Val Leu Val Leu Asp Ala Asn Asp Asn Ser Pro Phe Val Leu Tyr Pro 550	555	560	2454
CTG CAG AAC GGC TCC GCG CCC TGC ACC GAG CTG GTG CCC CGG GCG GCC Leu Gln Asn Gly Ser Ala Pro Cys Thr Glu Leu Val Pro Arg Ala Ala 565	570	575	2502
GAG CCG GGC TAC CTG GTG ACC AAG GTG GTG GCG GTG GAC GGC GAC TCG Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val Asp Gly Asp Ser 585	590	595	2550
GGC CAG AAC GCC TGG CTG TCG TAC CAG CTG CTC AAG GCC ACG GAG CCC Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Lys Ala Thr Glu Pro 600	605	610	2598
GGG CTG TTC GGC GTG TGG GCG CAC AAT GGC GAG GTG CGC ACC GCC AGG Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg 615	620	625	2646
CTG CTG AGC GAG CGC GAC GTG GCC AAG CAC AGG CTA GTG GTG CTG GTC Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu Val Val Leu Val 630	635	640	2694
AAG GAC AAT GGC GAG CCT CCG CGC TCG GCC ACA GCC ACG CTG CAA GTG Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Leu Gln Val 645	650	655	2742
CTC CTG GTG GAC GGC TTC TCT CAG CCC TAC CTG CCG CTC CCA GAG GCG Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu Ala 665	670	675	2790
GCC CCG GCC CAA GCC CAG GCC GAC TCG CTT ACC GTC TAC CTG GTG GTG Ala Pro Ala Gln Ala Gln Ala Asp Ser Leu Thr Val Tyr Leu Val Val 680	685	690	2838
GCA TTG GCC TCG GTG TCT TCG CTC TTC CTC TTC TCG GTG TTC CTG TTC Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val Phe Leu Phe 695	700	705	2886
GTG GCA GTG CGG CTG TGC AGG AGG AGC AGG GCG GCC TCA GTG GGT CGC Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala Ser Val Gly Arg 710	715	720	2934
TGC TCG GTG CCC GAG GGC CCC TTT CCA GGG CAT CTG GTG GAC GTG AGC Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu Val Asp Val Ser 725	730	735	2982
GGC ACC GGG ACC CTT TCC CAG AGC TAC CAG TAC GAG GTG TGT CTG ACG Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu Val Cys Leu Thr 745	750	755	3030

GGA GGC TCT GAA AGT AAT GAT TTC AAG TTC TTG AAG CCT ATA TTC CCA	3078
Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys Pro Ile Phe Pro	
760 765 770	
AAT ATT GTA AGC CAG GAC TCT AGG AGG AAA TCA GAA TTT CTA GAA	3123
Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu Phe Leu Glu	
775 780 785	
TAATGTAGGT ATCTGTAGCT TTCCGACCGT CTGTTAATTT TGTCTTCCTC ACTTTTCACC	3183
TTAGTTTTTT TTAACCCCTTT AGTAATCTTG AATTCTACTT TTTTTTAAAT TTCTACTGTT	3243
GTCTTTAGTA ATGTTACTCA TTTCCTTGT CTGATTGTTA GTTTTCAAAT TATTGTATTA	3303
TTATAAAATAT TTTATATCAG GAAAGTTCAT ATTTCTGAAT AAATTAATAG	3353

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Glu Pro Ala Gly Glu Arg Phe Pro Glu Gln Arg Gln Val Leu Ile	
1 5 10 15	
Leu Leu Leu Leu Glu Val Thr Leu Ala Gly Trp Glu Pro Arg Arg	
20 25 30	
Tyr Ser Val Met Glu Glu Thr Glu Arg Gly Ser Phe Val Ala Asn Leu	
35 40 45	
Ala Asn Asp Leu Gly Leu Gly Val Gly Glu Leu Ala Glu Arg Gly Ala	
50 55 60	
Arg Val Val Ser Glu Asp Asn Glu Gln Gly Leu Gln Leu Asp Leu Gln	
65 70 75 80	
Thr Gly Gln Leu Ile Leu Asn Glu Lys Leu Asp Arg Glu Lys Leu Cys	
85 90 95	
Gly Pro Thr Glu Pro Cys Ile Met His Phe Gln Val Leu Lys Lys	
100 105 110	
Pro Leu Glu Val Phe Arg Ala Glu Leu Leu Val Thr Asp Ile Asn Asp	
115 120 125	
His Ser Pro Glu Phe Pro Glu Arg Glu Met Thr Leu Lys Ile Pro Glu	
130 135 140	
Thr Ser Ser Leu Gly Thr Val Phe Pro Leu Lys Lys Ala Arg Asp Leu	
145 150 155 160	
Asp Val Gly Ser Asn Asn Val Gln Asn Tyr Asn Ile Ser Pro Asn Ser	
165 170 175	

His Phe His Val Ser Thr Arg Thr Arg Gly Asp Gly Arg Lys Tyr Pro
 180 185 190
 Glu Leu Val Leu Asp Thr Glu Leu Asp Arg Glu Glu Gln Ala Glu Leu
 195 200 205
 Arg Leu Thr Leu Thr Ala Val Asp Gly Gly Ser Pro Pro Arg Ser Gly
 210 215 220
 Thr Val Gln Ile Leu Ile Leu Val Leu Asp Ala Asn Asp Asn Ala Pro
 225 230 235 240
 Glu Phe Val Gln Ala Leu Tyr Glu Val Gln Val Pro Glu Asn Ser Pro
 245 250 255
 Val Gly Ser Leu Val Val Lys Val Ser Ala Arg Asp Leu Asp Thr Gly
 260 265 270
 Thr Asn Gly Glu Ile Ser Tyr Ser Leu Tyr Tyr Ser Ser Gln Glu Ile
 275 280 285
 Asp Lys Pro Phe Glu Leu Ser Ser Leu Ser Gly Glu Ile Arg Leu Ile
 290 295 300
 Lys Lys Leu Asp Phe Glu Thr Met Ser Ser Tyr Asp Leu Asp Ile Glu
 305 310 315 320
 Ala Ser Asp Gly Gly Leu Ser Gly Lys Cys Ser Val Ser Val Lys
 325 330 335
 Val Leu Asp Val Asn Asp Asn Phe Pro Glu Leu Ser Ile Ser Ser Leu
 340 345 350
 Thr Ser Pro Ile Pro Glu Asn Ser Pro Glu Thr Glu Val Ala Leu Phe
 355 360 365
 Arg Ile Arg Asp Arg Asp Ser Gly Glu Asn Gly Lys Met Ile Cys Ser
 370 375 380
 Ile Gln Asp Asp Val Pro Phe Lys Leu Lys Pro Ser Val Glu Asn Phe
 385 390 395 400
 Tyr Arg Leu Val Thr Glu Gly Ala Leu Asp Arg Glu Thr Arg Ala Glu
 405 410 415
 Tyr Asn Ile Thr Ile Thr Asp Leu Gly Thr Pro Arg Leu Lys
 420 425 430
 Thr Glu Gln Ser Ile Thr Val Leu Val Ser Asp Val Asn Asp Asn Ala
 435 440 445
 Pro Ala Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn
 450 455 460
 Ser Pro Ala Leu His Ile Gly Ser Val Ser Ala Thr Asp Arg Asp Ser
 465 470 475 480
 Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp Pro
 485 490 495

His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Thr Asp Asn Gly His
 500 505 510
 Leu Phe Ala Leu Gln Ser Leu Asp Tyr Glu Ala Leu Gln Ala Phe Glu
 515 520 525
 Phe Arg Val Gly Ala Thr Asp Arg Gly Phe Pro Ala Leu Ser Ser Glu
 530 535 540
 Ala Leu Val Arg Val Leu Val Leu Asp Ala Asn Asp Asn Ser Pro Phe
 545 550 555 560
 Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala Pro Cys Thr Glu Leu Val
 565 570 575
 Pro Arg Ala Ala Glu Pro Gly Tyr Leu Val Thr Lys Val Val Ala Val
 580 585 590
 Asp Gly Asp Ser Gly Gln Asn Ala Trp Leu Ser Tyr Gln Leu Leu Lys
 595 600 605
 Ala Thr Glu Pro Gly Leu Phe Gly Val Trp Ala His Asn Gly Glu Val
 610 615 620
 Arg Thr Ala Arg Leu Leu Ser Glu Arg Asp Val Ala Lys His Arg Leu
 625 630 635 640
 Val Val Leu Val Lys Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala
 645 650 655
 Thr Leu Gln Val Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro
 660 665 670
 Leu Pro Glu Ala Ala Pro Ala Gln Ala Asp Ser Leu Thr Val
 675 680 685
 Tyr Leu Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser
 690 695 700
 Val Phe Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala
 705 710 715 720
 Ser Val Gly Arg Cys Ser Val Pro Glu Gly Pro Phe Pro Gly His Leu
 725 730 735
 Val Asp Val Ser Gly Thr Gly Thr Leu Ser Gln Ser Tyr Gln Tyr Glu
 740 745 750
 Val Cys Leu Thr Gly Gly Ser Glu Ser Asn Asp Phe Lys Phe Leu Lys
 755 760 765
 Pro Ile Phe Pro Asn Ile Val Ser Gln Asp Ser Arg Arg Lys Ser Glu
 770 775 780
 Phe Leu Glu
 785

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3033 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 138..2528

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GTGATTGGAC GTGTTTTGT GACTATTTGG GAAGAAGACA CCTTCCTAAT CAGATTTACT	60
CCAATATCTT CCCGGACCCT CATGAGTGGA TTGCAATTGA CTTGAAGAAG CAGCACCCCTC	120
AGGACTGAAT CTGAACA ATG GAG ACA GCA CTA GCA AAA ATA CCA CAG CAA	170
Met Glu Thr Ala Leu Ala Lys Ile Pro Gln Gln	
1 5 10	
AGG CAA GTC TTT CTT ACT ATA TTG TCG TTA TTG TGG AAG TCT AGC	218
Arg Gln Val Phe Phe Leu Thr Ile Leu Ser Leu Leu Trp Lys Ser Ser	
15 20 25	
TCT GAG GCC ATT AGA TAT TCC ATG CCA GAA GAA ACA GAG AGT GGC TAT	266
Ser Glu Ala Ile Arg Tyr Ser Met Pro Glu Glu Thr Glu Ser Gly Tyr	
30 35 40	
ATG GTG GCT AAC CTG GCG AAA GAT CTG GGG ATC AGG GTT GGA GAA CTG	314
Met Val Ala Asn Leu Ala Lys Asp Leu Gly Ile Arg Val Gly Glu Leu	
45 50 55	
TCC TCT AGA GGA GCT CAA ATC CAT TAC AAA GGA AAC AAA GAA CTT TTG	362
Ser Ser Arg Gly Ala Gln Ile His Tyr Lys Gly Asn Lys Glu Leu Leu	
60 65 70 75	
CAG CTG GAT GCA GAG ACT GGG AAT TTG TTC TTA AAG GAA AAA CTA GAC	410
Gln Leu Asp Ala Glu Thr Gly Asn Leu Phe Leu Lys Glu Lys Leu Asp	
80 85 90	
AGA GAA CTG CTG TGT GGA GAG ACA GAA CCC TGT GTG CTG AAC TTC CAG	458
Arg Glu Leu Leu Cys Gly Glu Thr Glu Pro Cys Val Leu Asn Phe Gln	
95 100 105	
ATC ATA CTG GAA AAC CCT ATG CAG TTC TTC CAA ACT GAA CTG CAG CTC	506
Ile Ile Leu Glu Asn Pro Met Gln Phe Gln Thr Glu Leu Gln Leu	
110 115 120	
ACA GAT ATA AAC GAC CAT TCT CCA GAG TTC CCC AAC AAG AAA ATG CTT	554
Thr Asp Ile Asn Asp His Ser Pro Glu Phe Pro Asn Lys Lys Met Leu	
125 130 135	
CTA ACA ATT CCT GAG AGT GCC CAT CCA GGG ACT GTG TTT CCT CTG AAG	602
Leu Thr Ile Pro Glu Ser Ala His Pro Gly Thr Val Phe Pro Leu Lys	
140 145 150 155	

GCA GCT CGG GAC TCT GAC ATA GGG AGC AAC GCT GTT CAG AAC TAC ACA Ala Ala Arg Asp Ser Asp Ile Gly Ser Asn Ala Val Gln Asn Tyr Thr 160 165 170	650
GTC AAT CCC AAC CTC CAT TTC CAC GTC GTT ACT CAC AGT CGC ACA GAT Val Asn Pro Asn Leu His Phe His Val Val Thr His Ser Arg Thr Asp 175 180 185	698
GGC AGG AAA TAC CCA GAG CTG GTG CTG GAC AGA GCC CTG GAT AGG GAG Gly Arg Lys Tyr Pro Glu Leu Val Leu Asp Arg Ala Leu Asp Arg Glu 190 195 200	746
GAG CAG CCT GAG CTC ACT TTA ATC CTC ACT GCT CTG GAT GGT GGA GCT Glu Gln Pro Glu Leu Thr Leu Ile Leu Thr Ala Leu Asp Gly Gly Ala 205 210 215	794
CCT TCC AGG TCA GGA ACC ACC ACA GTT CAC ATA GAA GTT GTG GAC ATC Pro Ser Arg Ser Gly Thr Thr Val His Ile Glu Val Val Asp Ile 220 225 230 235	842
AAT GAT AAC TCC CCC CAG TTT GTA CAG TCA CTC TAT AAG GTG CAA GTT Asn Asp Asn Ser Pro Gln Phe Val Gln Ser Leu Tyr Lys Val Gln Val 240 245 250	890
CCT GAG AAT AAT CCC CTC AAT GCC TTT GTT GTC ACG GTC TCT GCC ACG Pro Glu Asn Asn Pro Leu Asn Ala Phe Val Val Thr Val Ser Ala Thr 255 260 265	938
GAT TTA GAT GCT GGG GTA TAT GGC AAT GTG ACC TAT TCT CTG TTT CAA Asp Leu Asp Ala Gly Val Tyr Gly Asn Val Thr Tyr Ser Leu Phe Gln 270 275 280	986
GGG TAT GGG GTA TTT CAA CCA TTT GTA ATA GAC GAA ATC ACT GGA GAA Gly Tyr Gly Val Phe Gln Pro Phe Val Ile Asp Glu Ile Thr Gly Glu 285 290 295	1034
ATC CAT CTG AGC AAA GAG CTG GAT TTT GAG GAA ATT AGC AAT CAT AAC Ile His Leu Ser Lys Glu Leu Asp Phe Glu Glu Ile Ser Asn His Asn 300 305 310 315	1082
ATA GAA ATC GCA GCC ACA GAT GGA GGA GGC CTT TCA GGA AAA TGC ACT Ile Glu Ile Ala Ala Thr Asp Gly Gly Leu Ser Gly Lys Cys Thr 320 325 330	1130
GTG GCT GTA CAG GTG TTG GAT GTG AAT GAC AAC GCC CCA GAG TTG ACA Val Ala Val Gln Val Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Thr 335 340 345	1178
ATT AGG AAG CTC ACA GTC CTG GTC CCA GAA AAT TCC GCA GAG ACT GTA Ile Arg Lys Leu Thr Val Leu Val Pro Glu Asn Ser Ala Glu Thr Val 350 355 360	1226
GTT GCT GTT TTT AGT GTT TCT GAT TCT GAT TCG GGG GAC AAT GGA AGG Val Ala Val Phe Ser Val Ser Asp Ser Gly Asp Asn Gly Arg 365 370 375	1274
ATG GTG TGT TCT ATT CCG AAC AAT ATC CCA TTT CTC CTG AAA CCC ACA Met Val Cys Ser Ile Pro Asn Asn Ile Pro Phe Leu Leu Lys Pro Thr 380 385 390 395	1322

TTT GAG AAT TAT TAC ACG TTA GTG ACT GAG GGG CCA CTT GAT AGA GAG Phe Glu Asn Tyr Tyr Thr Leu Val Thr Glu Gly Pro Leu Asp Arg Glu 400 405 410	1370
AAC AGA GCT GAG TAC AAC ATC ACC ATC ACG GTC TCA GAT CTG GGC ACA Asn Arg Ala Glu Tyr Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr 415 420 425	1418
CCC AGG CTC ACA ACC CAG CAC ACC ATA ACA GTG CAA GTG TCC GAC ATC Pro Arg Leu Thr Thr Gln His Thr Ile Thr Val Gln Val Ser Asp Ile 430 435 440	1466
AAC GAC AAC GCC CCT GCC TTC ACC CAA ACC TCC TAC ACC ATG TTT GTC Asn Asp Asn Ala Pro Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val 445 450 455	1514
CAC GAG AAC AAC AGC CCC GCC CTG CAC ATA GGC ACC ATC AGT GCC ACA His Glu Asn Asn Ser Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr 460 465 475	1562
GAC TCA GAC TCA GGC TCC AAT GCC CAC ATC ACC TAC TCG CTG CTG CCG Asp Ser Asp Ser Gly Ser Asn Ala His Ile Thr Tyr Ser Leu Leu Pro 480 485 490	1610
CCT GAT GAC CCG CAG CTG GCC CTC GAC TCA CTC ATC TCC ATC AAT GTT Pro Asp Asp Pro Gln Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Val 495 500 505	1658
GAC AAT GGG CAG CTG TTC GCG CTC AGA GCT CTA GAC TAT GAG GCA CTG Asp Asn Gly Gln Leu Phe Ala Leu Arg Ala Leu Asp Tyr Glu Ala Leu 510 515 520	1706
CAG TCC TTC GAG TTC TAC GTG GGC GCT ACA GAT GGA GGC TCA CCC GCG Gln Ser Phe Glu Phe Tyr Val Gly Ala Thr Asp Gly Ser Pro Ala 525 530 535	1754
CTC AGC AGC CAG ACT CTG GTG CGG ATG GTG GTG CTG GAT GAC AAT GAC Leu Ser Ser Gln Thr Leu Val Arg Met Val Val Leu Asp Asp Asn Asp 540 545 550 555	1802
AAT GCC CCC TTC GTG CTC TAC CCA CTG CAG AAT GCC TCA GCA CCC TGT Asn Ala Pro Phe Val Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Cys 560 565 570	1850
ACT GAG CTA CTG CCT AGG GCA GCA GAG CCC GGC TAC CTG ATC ACC AAA Thr Glu Leu Leu Pro Arg Ala Ala Glu Pro Gly Tyr Leu Ile Thr Lys 575 580 585	1898
GTG GTG GCT GTG GAT CGC GAC TCT GGA CAG AAT GCT TGG CTG TCG TTC Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe 590 595 600	1946
CAG CTA CTT AAA GCT ACA GAG CCA GGG CTG TTC AGT GTA TGG GCA CAC Gln Leu Leu Lys Ala Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His 605 610 615	1994
AAT GGT GAA GTG CGC ACC ACT AGG CTG CTG AGT GAG CGA GAT GCT CAG Asn Gly Glu Val Arg Thr Thr Arg Leu Leu Ser Glu Arg Asp Ala Gln 620 625 630 635	2042

AAG CAC AAG CTA CTG CTG GTC AAG GAC AAT GGC GAT CCT CTG CGC	2090
Lys His Lys Leu Leu Leu Val Lys Asp Asn Gly Asp Pro Leu Arg	
640 645 650	
TCT GCC AAT GTC ACT CTT CAC GTG CTA GTG GTG GAT GGC TTC TCG CAG	2138
Ser Ala Asn Val Thr Leu His Val Leu Val Val Asp Gly Phe Ser Gln	
655 660 665	
CCT TAC CTA CCA TTG GCT GAG GTG GCA CAG GAT TCC ATG CAA GAT AAT	2186
Pro Tyr Leu Pro Leu Ala Glu Val Ala Gln Asp Ser Met Gln Asp Asn	
670 675 680	
TAC GAC GTT CTC ACA CTG TAC CTA GTC ATT GCC TTG GCA TCT GTA TCT	2234
Tyr Asp Val Leu Thr Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser	
685 690 695	
TCT CTC TTC CTC TTG TCT GTA GTG CTG TTT GTG GGG GTG AGG CTG TGC	2282
Ser Leu Phe Leu Leu Ser Val Val Leu Phe Val Gly Val Arg Leu Cys	
700 705 710 715	
AGG AGG GCC AGG GAG GCC TCC TTG GGT GAC TAC TCT GTG CCT GAG GGA	2330
Arg Arg Ala Arg Glu Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly	
720 725 730	
CAC TTT CCT AGC CAC TTG GTG GAT GTC AGC GGT GCC GGG ACC CTG TCC	2378
His Phe Pro Ser His Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser	
735 740 745	
CAG AGT TAT CAA TAT GAG GTG TGT CTT AAT GGA GGT ACT AGA ACA AAT	2426
Gln Ser Tyr Gln Tyr Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn	
750 755 760	
GAG TTT AAC TTT CTT AAA CCA TTG TTT CCT ATC CTT CCG ACC CAG GCT	2474
Glu Phe Asn Phe Leu Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala	
765 770 775	
GCT GCT GCT GAA GAA AGA GAA AAC GCT GTT GTG CAC AAT AGC GTT GGA	2522
Ala Ala Ala Glu Glu Arg Glu Asn Ala Val Val His Asn Ser Val Gly	
780 785 790 795	
TTC TAT TAGAGCACTG ATTTTGAAGT GGTGGTTACC TCATTTTCC TTAACTATCC	2578
Phe Tyr	
CTGATGTAGA ATGGTGTAGT GCCGTGAATC AACTCCTGAG ATATATGTTA ATTTTATCCT	2638
TTGTTTGAA TCAAACATT CAGATGTGAT CCTACTCTAG AGAATTGTT TCTACTCCAT	2698
TGTGTTGTT TAGATTCTA CGCCATACCA GTGCATGCTG GGTTGTTTT TTTTTTACAA	2758
TTATTATAAC TTTGCTTGG AGGGAAACTC ATATTCGCTG TAACGAATTG GAACCACTTT	2818
CATTGTTAGA GATGCCCTGC TTTGTTGTGT TATTCAGAC AGGGTCTTAA ATTGTAGCCC	2878
TGGGTGACCT GAAATGACTA TGTACAGACT GACTTTGAAT TTGTGGCAGT CCATCTGCCT	2938
CTGTTGTCCT ATGTTGGAT TGTGAGCATG CATGAGTAGG CTCAGCTGTG GTGAGCGACC	2998
TTAATAAAAA TCAAATACTA AAAAAAAA AAAAA	3033

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 797 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Glu Thr Ala Leu Ala Lys Ile Pro Gln Gln Arg Gln Val Phe Phe
 1 5 10 15

Leu Thr Ile Leu Ser Leu Leu Trp Lys Ser Ser Ser Glu Ala Ile Arg
 20 25 30

Tyr Ser Met Pro Glu Glu Thr Glu Ser Gly Tyr Met Val Ala Asn Leu
 35 40 45

Ala Lys Asp Leu Gly Ile Arg Val Gly Glu Leu Ser Ser Arg Gly Ala
 50 55 60

Gln Ile His Tyr Lys Gly Asn Lys Glu Leu Leu Gln Leu Asp Ala Glu
 65 70 75 80

Thr Gly Asn Leu Phe Leu Lys Glu Lys Leu Asp Arg Glu Leu Leu Cys
 85 90 95

Gly Glu Thr Glu Pro Cys Val Leu Asn Phe Gln Ile Ile Leu Glu Asn
 100 105 110

Pro Met Gln Phe Phe Gln Thr Glu Leu Gln Leu Thr Asp Ile Asn Asp
 115 120 125

His Ser Pro Glu Phe Pro Asn Lys Lys Met Leu Leu Thr Ile Pro Glu
 130 135 140

Ser Ala His Pro Gly Thr Val Phe Pro Leu Lys Ala Ala Arg Asp Ser
 145 150 155 160

Asp Ile Gly Ser Asn Ala Val Gln Asn Tyr Thr Val Asn Pro Asn Leu
 165 170 175

His Phe His Val Val Thr His Ser Arg Thr Asp Gly Arg Lys Tyr Pro
 180 185 190

Glu Leu Val Leu Asp Arg Ala Leu Asp Arg Glu Glu Gln Pro Glu Leu
 195 200 205

Thr Leu Ile Leu Thr Ala Leu Asp Gly Gly Ala Pro Ser Arg Ser Gly
 210 215 220

Thr Thr Thr Val His Ile Glu Val Val Asp Ile Asn Asp Asn Ser Pro
 225 230 235 240

Gln Phe Val Gln Ser Leu Tyr Lys Val Gln Val Pro Glu Asn Asn Pro
 245 250 255

Leu Asn Ala Phe Val Val Thr Val Ser Ala Thr Asp Leu Asp Ala Gly
 260 265 270

val Tyr Gly Asn Val Thr Tyr Ser Leu Phe Gln Gly Tyr Gly Val Phe
 275 280 285
 Gln Pro Phe Val Ile Asp Glu Ile Thr Gly Glu Ile His Leu Ser Lys
 290 295 300
 Glu Leu Asp Phe Glu Glu Ile Ser Asn His Asn Ile Glu Ile Ala Ala
 305 310 315 320
 Thr Asp Gly Gly Leu Ser Gly Lys Cys Thr Val Ala Val Gln Val
 325 330 335
 Leu Asp Val Asn Asp Asn Ala Pro Glu Leu Thr Ile Arg Lys Leu Thr
 340 345 350
 Val Leu Val Pro Glu Asn Ser Ala Glu Thr Val Val Ala Val Phe Ser
 355 360 365
 Val Ser Asp Ser Asp Ser Gly Asp Asn Gly Arg Met Val Cys Ser Ile
 370 375 380
 Pro Asn Asn Ile Pro Phe Leu Leu Lys Pro Thr Phe Glu Asn Tyr Tyr
 385 390 395 400
 Thr Leu Val Thr Glu Gly Pro Leu Asp Arg Glu Asn Arg Ala Glu Tyr
 405 410 415
 Asn Ile Thr Ile Thr Val Ser Asp Leu Gly Thr Pro Arg Leu Thr Thr
 420 425 430
 Gln His Thr Ile Thr Val Gln Val Ser Asp Ile Asn Asp Asn Ala Pro
 435 440 445
 Ala Phe Thr Gln Thr Ser Tyr Thr Met Phe Val His Glu Asn Asn Ser
 450 455 460
 Pro Ala Leu His Ile Gly Thr Ile Ser Ala Thr Asp Ser Asp Ser Gly
 465 470 475 480
 Ser Asn Ala His Ile Thr Tyr Ser Leu Leu Pro Pro Asp Asp Pro Gln
 485 490 495
 Leu Ala Leu Asp Ser Leu Ile Ser Ile Asn Val Asp Asn Gly Gln Leu
 500 505 510
 Phe Ala Leu Arg Ala Leu Asp Tyr Glu Ala Leu Gln Ser Phe Glu Phe
 515 520 525
 Tyr Val Gly Ala Thr Asp Gly Gly Ser Pro Ala Leu Ser Ser Gln Thr
 530 535 540
 Leu Val Arg Met Val Val Leu Asp Asp Asn Asp Asn Ala Pro Phe Val
 545 550 555 560
 Leu Tyr Pro Leu Gln Asn Ala Ser Ala Pro Cys Thr Glu Leu Leu Pro
 565 570 575
 Arg Ala Ala Glu Pro Gly Tyr Leu Ile Thr Lys Val Val Ala Val Asp
 580 585 590

Arg Asp Ser Gly Gln Asn Ala Trp Leu Ser Phe Gln Leu Leu Lys Ala
 595 600 605
 Thr Glu Pro Gly Leu Phe Ser Val Trp Ala His Asn Gly Glu Val Arg
 610 615 620
 Thr Thr Arg Leu Leu Ser Glu Arg Asp Ala Gln Lys His Lys Leu Leu
 625 630 635 640
 Leu Leu Val Lys Asp Asn Gly Asp Pro Leu Arg Ser Ala Asn Val Thr
 645 650 655
 Leu His Val Leu Val Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu
 660 665 670
 Ala Glu Val Ala Gln Asp Ser Met Gln Asp Asn Tyr Asp Val Leu Thr
 675 680 685
 Leu Tyr Leu Val Ile Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Leu
 690 695 700
 Ser Val Val Leu Phe Val Gly Val Arg Leu Cys Arg Arg Ala Arg Glu
 705 710 715 720
 Ala Ser Leu Gly Asp Tyr Ser Val Pro Glu Gly His Phe Pro Ser His
 725 730 735
 Leu Val Asp Val Ser Gly Ala Gly Thr Leu Ser Gln Ser Tyr Gln Tyr
 740 745 750
 Glu Val Cys Leu Asn Gly Gly Thr Arg Thr Asn Glu Phe Asn Phe Leu
 755 760 765
 Lys Pro Leu Phe Pro Ile Leu Pro Thr Gln Ala Ala Ala Glu Glu
 770 775 780
 Arg Glu Asn Ala Val Val His Asn Ser Val Gly Phe Tyr
 785 790 795

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2347 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

AAAACACGGG GGAAATGACA GTAGCAAAGA ATCTGGACTA TGAAGAATGC TCATTGTATG	60
AAATGGAAAT ACAGGCTGAA GATGTGGGG CGCTTCTGGG GAGGAGCAAA GTGGTAATTA	120
TGGTAGAAGA TGTAAATGAC AATCGGCCAG AAGTGACCAT TACATCCTTG TTTAACCCGG	180
TATTGGAAAA TTCTCTTCCC GGGACAGTAA TTGCCTTCTT GAATGTGCAT GACCGAGACT	240
CTGGAAAGAA CGGCCAAGTT GTCTGTTACA CGCATGATAA CTTACCTTT AAATTAGAAA	300

AGTCAATAGA TAATTATTAT AGATTGGTGA CATGGAAATA TTTGGACCGA GAAAAAGTCT	360
CCATCTACAA TATCACAGTG ATAGCCTAG ATCTAGGAGC CCACCTCTGC ACTGAAACTT	420
ACATTGCCCT GATTGTGGCA GACACTAATG ACAACCCCTCC TCGTTTCCT CACACCTCCT	480
ACACAGCCTA TATTCCAGAG ACAAACCTGA GGGGCGCCTC CATCTTCTCA CTGACTGCAC	540
ATGATCCTGA CAGTCAGGAA AATGCACAGG TCACTTACTC TGTGTCTGAG GACACCATAAC	600
AGGGAGTGCC TTTGTCCCTCT TATATCTCCA TCAACTCAGA TACTGGTGTC CTGTATGCAC	660
TGCACTCTTT TGACTTCGAG AAGATAACAAG ACTTGCAGCT ACTGGTTGTT GCCACTGACA	720
GTGGAAGCCC ACCTCTCAGC AGCAATGTGT CATTGAGCTT GTTTGTGTTG GACCAGAACG	780
ACAACGCACC TGAGATTCTA TATCCTAGCT TCCCCACAGA TGGCTCCACT GGTGTGGAAC	840
TAGCACCCCG CTCTGCAGAG CCTGGATACC TAGTGACCAA AGTGGTGGCA GTGGACAAAG	900
ACTCAGGACA GAATGCTTGG CTGTCCTACC GTCTGCTGAA GGCCAGCGAA CCTGGGCTCT	960
TCTCTGTAGG ACTTCACACG GGTGAGGTGC GTACAGCGAG GGCCCTGCTG GACAGAGATG	1020
CTCTCAAACA GAATCTGGTG ATGGCCGTGC AGGACCATGG CCAACCCCT CTCTCGGCCA	1080
CTGTAACTCT CACTGTGGCA GTGGCTAACAA GCATCCCTGA GGTGTTGGCT GACTTGAGCA	1140
GCATTAGGAC CCCTGGGTA CCAGAGGATT CTGATATCAC GCTCCACCTG GTGGTGGCAG	1200
TGGCTGTGGT CTCCTGTGTC TTCCTTGTCT TTGTCATTGT CCTCCTAGCT CTCAGGCTTC	1260
AGCGCTGGCA GAAGTCTCGC CAGCTCCAGG GCTCCAAAGG TGGATTGGCT CCTGCACCTC	1320
CATCACATTT TGTGGGCATC GACGGGGTAC AGGCTTTCT ACAAACCTAT TCTCATGAAG	1380
TCTCGCTCAC TTCAGGCTCC CAGACAAGCC ACATTATCTT TCCTCAGCCC AACTATGCAG	1440
ACATGCTCAT TAACCAAGAA GGCTGTGAGA AAAATGATTC CTTATTAACA TCCATAGATT	1500
TTCATGAGAG TAACCGTGAA GATGCTTGC GCGGATCCC CCCGCCAAC ACTGACTGGC	1560
GTTTCTCTCA AGCCCAGAGA CCCGGCACGA GCGGATCCC AAATGGGGAT GAAACCGGCA	1620
CCTGGCCCAA CAACCAGTTC GATACAGAGA TGCTGCAAGC CATGATTTG GCCTCTGCCA	1680
GTGAAGCCGC TGATGGGAGC TCCACTCTGG GAGGGGGCAC TGGCACTATG GGTTTGAGCG	1740
CTCGATATGG ACCCCAGTTT ACCCTGCAGC ACGTGCCTGA CTACCGCCAG AACGTGTACA	1800
TCCCTGGCAG CAATGCCACA CTGACCAACG CAGCTGGCAA ACGAGATGGC AAGGCTCCGG	1860
CAGGCGGCAA TGGCAACAAC AACAAAGTCGG GCAAGAAAGA GAAGAAGTAA TATGGAGGCC	1920
AGGCCTTGAG CCACAGGGCA GCCTCCCTCC CCAGCCAGTC CAGCTTGTC TTACTTGTAC	1980
CCAGGCCTCA GAATTCAGG GCTCACCCCA GGATTCTGGT AGGAGCCACA GCCAGGCCAT	2040
GCTCCCCGTT GGGAAACAGA AACAAAGTGC CAAAGCCAACA CCCCCTCTTT GTACCCCTAGG	2100
GGGGTTGAAT ATGCAAAGAG AGTTCTGCTG GGACCCCTA TCCAATCAGT GATTGTACCC	2160

ACATAGGTAG CAGGGTTAGT GTGGATACAC ACACACACAC ACACACACAC	2220
CCCTTGTCCCT CCGCAGTGCC TGCCACTTTC TGGGACTTTC TCATCCCCCT ACGCCCTTCC	2280
TTTATCCTCT CCCACCCAGA CACAGCTGCT GGAGAATAAA TTTGGGGATG CTGATGCTAA	2340
AAAAAAAAA	2347

(2) INFORMATION FOR SEQ ID NO:114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2972 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..1849

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

A GAG GCT GCT CAC CAC CTG GTC CTC ACG GCC TCG GAT GGC GGC AAG	46
Glu Ala Ala His His Leu Val Leu Thr Ala Ser Asp Gly Gly Lys	
1 5 10 15	
CCG CCT CGC TCT AGC ACA GTG CGC ATC CAC GTG ACA GTG TTG GAT ACA	94
Pro Pro Arg Ser Ser Thr Val Arg Ile His Val Thr Val Leu Asp Thr	
20 25 30	
AAT GAC AAT GCC CCG GTT TTT CCT CAC CCG ATT TAC CGA GTG AAA GTC	142
Asn Asp Asn Ala Pro Val Phe Pro His Pro Ile Tyr Arg Val Lys Val	
35 40 45	
CTT GAG AAC ATG CCC CCA GGC ACG CGG CTG CTT ACT GTA ACA GCC AGC	190
Leu Glu Asn Met Pro Pro Gly Thr Arg Leu Leu Thr Val Thr Ala Ser	
50 55 60	
GAC CCG GAT GAG GGA ATC AAC GGA AAA GTG GCA TAC AAA TTC CGG AAA	238
Asp Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys	
65 70 75	
ATT AAT GAA AAA CAA ACT CCG TTA TTC CAG CTT AAT GAA AAT ACT GGG	286
Ile Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly	
80 85 90 95	
GAA ATA TCA ATA GCA AAA AGT CTA GAT TAT GAA GAA TGT TCA TTT TAT	334
Glu Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr	
100 105 110	
GAA ATG GAA ATA CAA GCC GAA GAT GTG GGG GCA CTT CTG GGG AGG ACC	382
Glu Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr	
115 120 125	
AAA TTG CTC ATT TCT GTG GAA GAT GTA AAT GAC AAT AGA CCA GAA GTG	430
Lys Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val	
130 135 140	

ATC ATT ACG TCT TTG TTT AGC CCA GTG TTA GAA AAT TCT CTT CCC GGG Ile Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly 145 150 155	478
ACA GTA ATT GCC TTC TTG AGT GTG CAT GAC CAA GAC TCT GGA AAG AAT Thr Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn 160 165 170 175	526
GGT CAA GTT GTC TGT TAC ACA CGT GAT AAT TTA CCT TTT AAA TTA GAA Gly Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu 180 185 190	574
AAG TCA ATA GGT AAT TAT TAT AGA TTA GTG ACA AGG AAA TAT TTG GAC Lys Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp 195 200 205	622
CGA GAA AAT GTC TCT ATC TAC AAT ATC ACA GTG ATG GCC TCA GAT CTA Arg Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu 210 215 220	670
GGA ACA CCA CCT CTG TCC ACT GAA ACT CAA ATC GCT CTG CAC GTG GCA Gly Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala 225 230 235	718
GAC ATT AAC GAC AAC CCT CCT ACT TTC CCT CAT GCC TCC TAC TCA GCG Asp Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala 240 245 250 255	766
TAT ATC CTA GAG AAC AAC CTG AGA GGA GCC TCC ATC TTT TCC TTG ACT Tyr Ile Leu Glu Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr 260 265 270	814
GCA CAC GAC CCC GAC AGC CAG GAG AAT GCC CAG GTC ACT TAC TCT GTG Ala His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val 275 280 285	862
ACC GAG GAC ACG CTG CAG GGG GCG CCC CTG TCC TCG TAT ATC TCC ATC Thr Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile 290 295 300	910
AAC TCT GAC ACC GGT GTC CTG TAT GCG CTG CAA TCT TTC GAC TAT GAG Asn Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu 305 310 315	958
CAG ATC CGA GAC CTG CAG CTA CTG GTA ACA GCC AGC GAC AGC GGG GAC Gln Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp 320 325 330 335	1006
CCG CCC CTC AGC AGC AAC ATG TCA CTG AGC CTG TTC GTG CTG GAC CAG Pro Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln 340 345 350	1054
AAT GAC AAC GCG CCC GAG ATC CTG TAC CCC GCC CTC CCC ACA GAC GGT Asn Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly 355 360 365	1102
TCC ACT GGC GTG GAG CTG GCG CCC CGC TCC GCA GAG CGT GGC TAC CTG Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu 370 375 380	1150

GTG ACC AAG GTG GTG GCG GTG GAC AGA GAC TCG GGC CAG AAC GCC TGG		1198
Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp		
385 390 395		
CTG TCC TAC CGC CTG CTC AAG GCC AGC GAG CCG GGA CTC TTC TCG GTG		1246
Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val		
400 405 410 415		
GGT CTG CAC ACG GGC GAG GTG CGC ACG GCG CGA GCC CTG CTG GAC AGA		1294
Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg		
420 425 430		
GAC GCG CTC AAG CAG AGC CTC GTG GTG GCC GTC CAG GAC CAT GGC CAG		1342
Asp Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln		
435 440 445		
CCC CCT CTC TCC GCC ACT GTC ACG CTC ACC GTA GCC GTG GCT GAC AGC		1390
Pro Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser		
450 455 460		
ATC CCC GAA GTC CTG ACC GAG TTG GGC AGT CTG AAG CCT TCG GTC GAC		1438
Ile Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp		
465 470 475		
CCG AAC GAT TCG AGC CTT ACA CTC TAT CTC GTG GTG GCA GTG GCT GCC		1486
Pro Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala		
480 485 490 495		
ATC TCC TGT GTC TTC CTC GCC TTT GTC GCT GTG CTT CTG GGG CTC AGG		1534
Ile Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg		
500 505 510		
CTG AGG CGC TGG CAC AAG TCA CGC CTG CTC CAG GAT TCC GGT GGC AGA		1582
Leu Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg		
515 520 525		
TTG GTA GGC GTG CCT GCC TCA CAT TTT GTG GGT GTT GAG GAG GTA CAG		1630
Leu Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln		
530 535 540		
GCT TTC CTG CAG ACC TAT TCC CAG GAA GTC TCC CTC ACC GCC GAC TCG		1678
Ala Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser		
545 550 555		
CGG AAG AGT CAC CTG ATC TTT CCC CAG CCC AAC TAC GCA GAC ATG CTC		1726
Arg Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu		
560 565 570 575		
ATC AGT CAG GAG GGC TGT GAG AAA AAT GAT TCT TTG TTA ACA TCC GTA		1774
Ile Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val		
580 585 590		
GAT TTT CAT GAA TAT AAG AAT GAA GCT GAT CAT GGT CAG GTG AGT TTA		1822
Asp Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu		
595 600 605		
GTT CTT TGC TTG CTT TTA ATT TCC AGA TGAATTTAT TTGGCATAAA		1869
Val Leu Cys Leu Leu Ile Ser Arg		
610 615		

TTATGTTTG AAAAACATTG TGAAGATAGT TGAAAATAAT TTTTAAGGTG TATCACAGAG	1929
TTTTGGTTT ATTTGGTGG TGTTACCAAA AAATTGAAC TTAATAGTCA TAGGTTATTG	1989
TTTCATTGCA TTTTAAACGA CTTGGAAAAG ATTGTTCCAC CATTAAAC CTTCCAGTAT	2049
TTTATTCCCTA TTATCACTCA TTCACCTAAG AAGTAGCTAC CCGTCCATAC TGGTAATTG	2109
GCTATTGTTT GTTTGTGTGT GTGTGTGTGT GTGTGTGTAT CCCAAACTAG	2169
AACTTCAGAA AATTATCAAG AAGTCTAAAG CTTGTTATT AGCTTAGCAA AAGTAAATA	2229
TATCTCAGAA TTTTAGGGT TATGTTAGC ATTTGAACCT GTAACTAGGC TCTTGTATAT	2289
TTCTTCACCT TAAACCTCTT TTCTGAGCCC TGTTCTGTA CCAGTGCCT TCAAAACTTT	2349
AATACTTCTT ACCATCCTTC AAAACATGAA CAAACTTAA AGATGGATCT TGGTGGGAGA	2409
TGAGACTGGT TACTAAATAT TAAGTATGTG AGTCAGTGGT CACCTGGCCT CCATCCCCAT	2469
GGAGACATGA AATCTAAAGC CTAGAATGTC CATTGCTCCC CCAAACAAAA AACAAAAGCA	2529
AAAACATTAG ATCTGAATTA AAATGTAATT TTAAACTGTT GAAAGTGAAT TTTGTAAT	2589
ATGTAAGAAC ATATTCAA ACAATTCAA TTAGCTGTT CGGTTGTGCA TTGATGTGAA	2649
GTGGTGAGAA TGTTGATATT AAGAACCAAT GTTTCAGGTA CACAAGTTCT AAATAAGCTG	2709
ATCAATTCAA TTAAAGTTAT TCAGTCTTGG CTGGACACAG TGCCTCATGT CTGAAATCCC	2769
AGCACTTGG GAGGCTGGGG CAGGAGGACC GCTTGAGCCC CGGGGGTTTG AACTGCAGT	2829
GAGCTATGAT CATGCCACTG CACTCCAGCC TAGGTGGCAG AACTAGACCC TGTCTCTAAA	2889
AAAACATTAA TTAGGCCGCG TGCGGTGGCT CACGCCCTGTA ATCCCAGCAC TTTGGGAGAC	2949
TGAGGTGGGT GGATCACCTG AGC	2972

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 616 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Glu	Ala	Ala	His	His	Leu	Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Lys	Pro
1					5				10					15	

Pro	Arg	Ser	Ser	Thr	Val	Arg	Ile	His	Val	Thr	Val	Leu	Asp	Thr	Asn
					20				25				30		

Asp	Asn	Ala	Pro	Val	Phe	Pro	His	Pro	Ile	Tyr	Arg	Val	Lys	Val	Leu
									35			40		45	

Glu	Asn	Met	Pro	Pro	Gly	Thr	Arg	Leu	Leu	Thr	Val	Thr	Ala	Ser	Asp
									50			55		60	

Pro Asp Glu Gly Ile Asn Gly Lys Val Ala Tyr Lys Phe Arg Lys Ile
 65 70 75 80
 Asn Glu Lys Gln Thr Pro Leu Phe Gln Leu Asn Glu Asn Thr Gly Glu
 85 90 95
 Ile Ser Ile Ala Lys Ser Leu Asp Tyr Glu Glu Cys Ser Phe Tyr Glu
 100 105 110
 Met Glu Ile Gln Ala Glu Asp Val Gly Ala Leu Leu Gly Arg Thr Lys
 115 120 125
 Leu Leu Ile Ser Val Glu Asp Val Asn Asp Asn Arg Pro Glu Val Ile
 130 135 140
 Ile Thr Ser Leu Phe Ser Pro Val Leu Glu Asn Ser Leu Pro Gly Thr
 145 150 155 160
 Val Ile Ala Phe Leu Ser Val His Asp Gln Asp Ser Gly Lys Asn Gly
 165 170 175
 Gln Val Val Cys Tyr Thr Arg Asp Asn Leu Pro Phe Lys Leu Glu Lys
 180 185 190
 Ser Ile Gly Asn Tyr Tyr Arg Leu Val Thr Arg Lys Tyr Leu Asp Arg
 195 200 205
 Glu Asn Val Ser Ile Tyr Asn Ile Thr Val Met Ala Ser Asp Leu Gly
 210 215 220
 Thr Pro Pro Leu Ser Thr Glu Thr Gln Ile Ala Leu His Val Ala Asp
 225 230 235 240
 Ile Asn Asp Asn Pro Pro Thr Phe Pro His Ala Ser Tyr Ser Ala Tyr
 245 250 255
 Ile Leu Glu Asn Asn Leu Arg Gly Ala Ser Ile Phe Ser Leu Thr Ala
 260 265 270
 His Asp Pro Asp Ser Gln Glu Asn Ala Gln Val Thr Tyr Ser Val Thr
 275 280 285
 Glu Asp Thr Leu Gln Gly Ala Pro Leu Ser Ser Tyr Ile Ser Ile Asn
 290 295 300
 Ser Asp Thr Gly Val Leu Tyr Ala Leu Gln Ser Phe Asp Tyr Glu Gln
 305 310 315 320
 Ile Arg Asp Leu Gln Leu Leu Val Thr Ala Ser Asp Ser Gly Asp Pro
 325 330 335
 Pro Leu Ser Ser Asn Met Ser Leu Ser Leu Phe Val Leu Asp Gln Asn
 340 345 350
 Asp Asn Ala Pro Glu Ile Leu Tyr Pro Ala Leu Pro Thr Asp Gly Ser
 355 360 365
 Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Arg Gly Tyr Leu Val
 370 375 380

Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln Asn Ala Trp Leu
 385 390 395 400
 Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly Leu Phe Ser Val Gly
 405 410 415
 Leu His Thr Gly Glu Val Arg Thr Ala Arg Ala Leu Leu Asp Arg Asp
 420 425 430
 Ala Leu Lys Gln Ser Leu Val Val Ala Val Gln Asp His Gly Gln Pro
 435 440 445
 Pro Leu Ser Ala Thr Val Thr Leu Thr Val Ala Val Ala Asp Ser Ile
 450 455 460
 Pro Glu Val Leu Thr Glu Leu Gly Ser Leu Lys Pro Ser Val Asp Pro
 465 470 475 480
 Asn Asp Ser Ser Leu Thr Leu Tyr Leu Val Val Ala Val Ala Ala Ile
 485 490 495
 Ser Cys Val Phe Leu Ala Phe Val Ala Val Leu Leu Gly Leu Arg Leu
 500 505 510
 Arg Arg Trp His Lys Ser Arg Leu Leu Gln Asp Ser Gly Gly Arg Leu
 515 520 525
 Val Gly Val Pro Ala Ser His Phe Val Gly Val Glu Glu Val Gln Ala
 530 535 540
 Phe Leu Gln Thr Tyr Ser Gln Glu Val Ser Leu Thr Ala Asp Ser Arg
 545 550 555 560
 Lys Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Ile
 565 570 575
 Ser Gln Glu Gly Cys Glu Lys Asn Asp Ser Leu Leu Thr Ser Val Asp
 580 585 590
 Phe His Glu Tyr Lys Asn Glu Ala Asp His Gly Gln Val Ser Leu Val
 595 600 605
 Leu Cys Leu Leu Ile Ser Arg
 610 615